

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 23, 2005, 12:39:59 ; Search time 51.1475 Seconds

300.354 Million cell updates/sec
(without alignments)

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5
Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:

1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1		147	100.0	150	2	Q9c001	homo sapien
2		147	100.0	153	1	IL2_HUMAN	
3		147	100.0	153	1	IL2_HYLIA	
4		147	100.0	153	2	Q61z93	homo sapien
5		147	100.0	154	1	IL2_MACPA	
6		147	100.0	154	1	IL2_MACNU	
7		147	100.0	154	1	IL2_MACNE	
8		147	100.0	154	1	IL2_PAPAN	
9		145	98.6	154	1	IL2_SAISC	
10		145	98.6	154	2	Q7Jfm2	actus lemuri
11		145	98.6	154	2	Q7Jfm3	actus nigri
12		145	98.6	154	2	Q7Jfm4	actus vocif
13		145	98.6	154	2	Q7Jfm5	actus nancy
14		145	98.6	154	2	Q9x838	papio hamad
15		143	97.3	133	2	Q6QWNO	homo sapien
16		143	97.3	133	2	Q7ZTm3	homo sapien
17		142	96.6	154	1	IL2_FELCA	
18		137	93.2	153	1	Q6N791	cercocetus
19		135.5	92.2	156	2	Q13169	homo sapien
20		134	91.2	139	2	Q16334	homo sapien
21		116	78.9	154	1	IL2_MIRAN	
22		114	77.6	154	1	IL2_FELCA	
23		109.5	73.8	155	2	Q9x783	halichoerus
24		107.5	73.1	66	1	Q9BG74	canis famili
25		107	73.1	155	1	IL2_CANPA	
26		107	72.8	79	2	Q9TV12	canis famili
27		107	72.8	152	1	Q8OK33	peromyscus
28		107	72.8	153	1	IL2_RABIT	
29		106	72.1	133	2	Q9mZ9	oryctolagrus
30		106	72.1	155	2	Q923T2	sigmodon hi
31		103	70.1	138	2	070329	mesocricetus

RESULT 1

Q9C001 PRELIMINARY; PRT; 150 AA.
ID Q9C001;
AC Q9C001;
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
OS Homo sapiens (Human).
OC Mammalia; Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN RP SEQUENCE FROM N.A.
RX MEDLINE=20545237; PubMed=11093171;
RX DOI=10.1002/1529-4141(200012)30:12<3516::AID-IMMU3516>3.0.CO;2-S;
RA Matseranz F.; Delgado C.; Freano M.; Aljina A.;
RT "Allelic selection of human IL-2 gene.";
RL EMBL: AF228636; AAG33575.1; -.
DR HSSP; P0566; IIRL.
DR GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
DR GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR0265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM0189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
FT NON_TER
SQ SEQUENCE 150 AA; 17312 MW;
SEQUENCE 150 AA; 17312 MW;
Query Match 100.0%; Score 147; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 5.1e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

IL2_HUMAN

GN Homo sapiens (Human).
ID IL2_HUMAN STANDARD; PRT; 153 AA.
AC P60568; P01585;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DB Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
DE (Adesleukin).
GN Name=IL2;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN RP SEQUENCE FROM N.A.
RX MEDLINE=34247453; PubMed=6330695;
RA Holbrook N.J.; Lieber M.; Crabtree G.R.;
RA "DNA sequence of the 5' flanking region of the human interleukin 2 gene: homologies with adult T-cell leukemia virus.";
RT Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
RN Name=IL2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN RP SEQUENCE FROM N.A.
RX MEDLINE=3167472; PubMed=6403867;
RA Taniguchi T.; Matsumi H.; Fujita T.; Takaoka C.; Kashima N.;
RA Yoshimoto T.; Hamuro J.;
RA "Structure and expression of a cloned cDNA for human interleukin-2.";
RT Nature 302:305-310(1983).
RN RP SEQUENCE FROM N.A.
RA Maeda S.; Nishino N.; Obara K.; Mita S.; Nomiyama H.; Shimada K.;
RA Fujimoto K.; Teranishi T.; Hirano T.; Ono K.;
RL Biochem. Biophys. Res. Commun. 115:1040-1047(1983).
[4]

SEQUENCE FROM N.A.
RN RP SEQUENCE FROM N.A.
RX MEDLINE=83246551; PubMed=6306584;
RA Devos R.; Plaetinck G.; Cherautre H.; Simons G.; Degrave W.;
RA Tavernier J.; Remaut E.; Fiers W.;
RA "Molecular cloning of human interleukin 2 cDNA and its expression in E. coli.";
RT Nucleic Acids Res. 11:4307-4323(1983).
RN RP SEQUENCE FROM N.A.
RX MEDLINE=84170356; PubMed=6608729;
RA Holbrook N.J.; Smith K.A.; Forncie A.J. Jr.; Comeau C.M.,
RA Wiskocil R.L.; Crabtree G.R.;
RT "T-cell growth factor: complete nucleotide sequence and organization of the gene in normal and malignant cells.";
RT Proc. Natl. Acad. Sci. U.S.A. 81:1634-1638(1984).
RN RP SEQUENCE FROM N.A.
RX MEDLINE=84170243; PubMed=6324170;
RA Fujita T.; Takaoka C.; Matsui H.; Taniguchi T.;
RA Bizenberg O.; Faber-Elman A.; Lotan M.; Schwartz M.;
RT "Structure of the human interleukin 2 gene.";
RT Proc. Natl. Acad. Sci. U.S.A. 80:7437-7441(1983).
RN RP SEQUENCE FROM N.A.
RX MEDLINE=95239150; PubMed=7722480;
RA Bizenberg O.; Faber-Elman A.; Lotan M.; Schwartz M.;
RT "Interleukin-2 transcripts in human and rodent brains: possible expression by astrocytes.";
RT Proc. Natl. Acad. Sci. U.S.A. 80:7437-7441(1983).
RN RP SEQUENCE FROM N.A.
RX MEDLINE=96422299; PubMed=8824916;
RA DOI=10.1002/(SICI)1098-2795(199602)43:2<180::AID-MRD7>3.3.CO;2-D;
RA Chernicky C.L.; Tan H.; Burfeind P.; Ilan J.; Ilan J.;
RA "Sequence of interleukin-2 isolated from human placental poly A+ RNA: possible role in maintenance of fetal allograft.";
RT J. Neurochem. 64:1928-1936(1995).
RN RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RA Nickerson D.A.;
RT "SeattleSNPs: NHLBI HL66682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu/>).";
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubberg R.L.; Feingold B.A.; Grouse L.H.; Derge J.G.;
RA Altschuler R.D.; Collins P.S.; Wagner L.; Schueler G.D.,
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh P.;
RA Diatchenko L.; Marusina K.; Farmer M.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prague C.;
RA Raha S.S.; Loqueland N.A.; Peters G.J.; Abramson R.D.; Mulahy S.J.;
RA Bosak S.A.; McEwan P.J.; McErlean K.J.; Malek J.A.; Gunnarson P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.,
RA Fahay J.; Helton B.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.,
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.,
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;
RA Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smialus D.B.,
RA Schenck A.; Schein J.E.; Jones S.J.M.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

Page 3

RT and mouse cDNA sequences.";	CC
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	CC
[11]	CC
SEQUENCE OF 21-153 FROM N.A.	CC
MEDLINE=89062420; PubMed=264184;	CC
RA Weir M.P., Chaplin M.A., Wallace D.M., Dykes C.W., Hobden A.N.;	CC
RT "Structure-activity relationships of recombinant human interleukin 2.";	CC
RT Biochemistry 27:6883-6892 (1988).	CC
[12]	CC
SEQUENCE OF 1-69 FROM N.A.	CC
MEDLINE=8064618; PubMed=3491296;	CC
RA Siebenlist U., Durand D.B., Brässler P., Holbrook N.J., Norris C.A.,	CC
RA Kamoun M., Kant J.A., Crabtree G.R.;	CC
RT "Promoter region of interleukin-2 gene undergoes chromatin structure changes and confers inducibility on chloramphenicol acetyltransferase gene during activation of T cells.";	CC
RT Mol. Cell. Biol. 6:3042-3049 (1986).	CC
[13]	CC
SEQUENCE OF 1-68 FROM N.A.	CC
RA Nishino N., Obara K., Maeda S., Shimada K., Onoue K.;	CC
RT "Organization of the DNA regions flanking the human interleukin 2 gene.";	CC
RT Biomed. Res. 6:197-205 (1995).	CC
[14]	CC
SEQUENCE OF 21-153, DISULFIDE BOND, AND CARBOHYDRATE-LINKAGE SITE.	CC
MEDLINE=89038540; PubMed=6333684;	CC
RA Robb R.J., Kutny R.M., Panico M., Morris H.R., Choudhry V.;	CC
RT "Amino acid sequence and post-translational modification of human interleukin 2.";	CC
RT Proc. Natl. Acad. Sci. U.S.A. 81:6486-6490 (1984).	CC
[15]	CC
CARBOHYDRATE-LINKAGE SITE.	CC
MEDLINE=90008901; PubMed=793860;	CC
RA Conradt H.S., Nimitz M., Dittmar K.E.J., Lindenmaier W., Hoppe J.,	CC
RA Hauser H.;	CC
RT "Expression of human interleukin-2 in recombinant baby hamster kidney, Ltk- and Chinese hamster ovary cells. Structure of O-linked carbohydrate chains and their location within the polypeptide.";	CC
RT J. Biol. Chem. 264:17368-17373 (1989).	CC
[16]	CC
X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).	CC
MEDLINE=88070616; PubMed=3500315;	CC
RA Brandhuber B.J., Boone T., Kenney W.C., McKay D.B.;	CC
RT "Three-dimensional structure of interleukin-2.";	CC
RT Science 238:1707-1709 (1987).	CC
[17]	CC
COMPARISON OF X-RAY STRUCTURES.	CC
MEDLINE=93335891; PubMed=1631562;	CC
RA Bazan J.F.;	CC
RT "Unraveling the structure of IL-2.";	CC
RT Science 238:410-412 (1992).	CC
[18]	CC
RESPONSE TO ABOVE LETTER.	CC
RA McKay D.B.;	CC
RA Science 257:412-413 (1992).	CC
[19]	CC
STRUCTURE BY NMR.	CC
MEDLINE=93279010; PubMed=1510960;	CC
RA Mott H.R., Driscoll P.C., Boyd J., Cooke R.M., Weir M.P.,	CC
RA Campbell J.D.;	CC
RT "Secondary structure of human interleukin 2 from 3D heteronuclear NMR modelling.";	CC
RT Biochemistry 31:7741-7744 (1992).	CC
[20]	CC
3D-STRUCTURE MAPPING.	CC
MEDLINE=93111955; PubMed=7529123;	CC
RA Bamforth P., Hedgecock C.J., Richards W.G.;	CC
RT "The interleukin-2 and interleukin-4 receptors studied by molecular modelling.";	CC
RT Structure 2:839-851 (1994).	CC
[21]	CC
MICROGENIC SIMULATION.	CC
Produced by T-cells in response to antigenic or mitogenic stimulation this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.	CC
SUBCELLULAR LOCATION: Secreted.	CC
- SIMILARITY: Belongs to the IL-2 family.	CC
[22]	CC
SEQUENCE OF 1-111 FROM N.A.	CC
MEDLINE=89062420; PubMed=264184;	CC
RA Weir M.P., Chaplin M.A., Wallace D.M., Dykes C.W., Hobden A.N.;	CC
RT "Structure-activity relationships of recombinant human interleukin 2.";	CC
RT Biochemistry 27:6883-6892 (1988).	CC
[23]	CC
SEQUENCE OF 1-69 FROM N.A.	CC
MEDLINE=8064618; PubMed=3491296;	CC
RA Siebenlist U., Durand D.B., Brässler P., Holbrook N.J., Norris C.A.,	CC
RA Kamoun M., Kant J.A., Crabtree G.R.;	CC
RT "Promoter region of interleukin-2 gene undergoes chromatin structure changes and confers inducibility on chloramphenicol acetyltransferase gene during activation of T cells.";	CC
RT Mol. Cell. Biol. 6:3042-3049 (1986).	CC
[24]	CC
SEQUENCE OF 1-68 FROM N.A.	CC
RA Nishino N., Obara K., Maeda S., Shimada K., Onoue K.;	CC
RT "Organization of the DNA regions flanking the human interleukin 2 gene.";	CC
RT Biomed. Res. 6:197-205 (1995).	CC
[25]	CC
SEQUENCE OF 21-153, DISULFIDE BOND, AND CARBOHYDRATE-LINKAGE SITE.	CC
MEDLINE=89038540; PubMed=6333684;	CC
RA Robb R.J., Kutny R.M., Panico M., Morris H.R., Choudhry V.;	CC
RT "Amino acid sequence and post-translational modification of human interleukin 2.";	CC
RT Proc. Natl. Acad. Sci. U.S.A. 81:6486-6490 (1984).	CC
[26]	CC
CARBOHYDRATE-LINKAGE SITE.	CC
MEDLINE=90008901; PubMed=793860;	CC
RA Conradt H.S., Nimitz M., Dittmar K.E.J., Lindenmaier W., Hoppe J.,	CC
RA Hauser H.;	CC
RT "Expression of human interleukin-2 in recombinant baby hamster kidney, Ltk- and Chinese hamster ovary cells. Structure of O-linked carbohydrate chains and their location within the polypeptide.";	CC
RT J. Biol. Chem. 264:17368-17373 (1989).	CC
[27]	CC
X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).	CC
MEDLINE=88070616; PubMed=3500315;	CC
RA Brandhuber B.J., Boone T., Kenney W.C., McKay D.B.;	CC
RT "Three-dimensional structure of interleukin-2.";	CC
RT Science 238:1707-1709 (1987).	CC
[28]	CC
STRUCTURE BY NMR.	CC
MEDLINE=93279010; PubMed=1510960;	CC
RA Mott H.R., Driscoll P.C., Boyd J., Cooke R.M., Weir M.P.,	CC
RA Campbell J.D.;	CC
RT "Secondary structure of human interleukin 2 from 3D heteronuclear NMR modelling.";	CC
RT Biochemistry 31:7741-7744 (1992).	CC
[29]	CC
3D-STRUCTURE MAPPING.	CC
MEDLINE=93111955; PubMed=7529123;	CC
RA Bamforth P., Hedgecock C.J., Richards W.G.;	CC
RT "The interleukin-2 and interleukin-4 receptors studied by molecular modelling.";	CC
RT Structure 2:839-851 (1994).	CC

CC	EMBL; M1144; AAP03454.1; -.	DR	InterPro; IPR000779; Interleukin-2.
DR	PTB1; A94067; ICG12.	DR	PFam; PF00715; IL2; 1.
DR	InterPro; IPR000779; Interleukin-2.	DR	PRINTS; PR00265; INTERLEUKIN2.
DR	PRINTS; PR00715; IL2; 1.	DR	ProDom; PD003619; Interleukin-2; 1.
DR	PRINTS; PR00265; INTERLEUKIN2.	DR	SMART; SM00189; IL2; 1.
DR	ProDom; PD003649; Interleukin-2; 1.	DR	PROSITE; PS00424; INTERLEUKIN-2; 1.
DR	SMART; SM00189; IL2; 1.	DR	SEQUENCE; 153 AA; 17597 MW; 1942F50F25960E88 CRC64;
DR	PROSITE; PS00424; INTERLEUKIN 2; 1.	Query Match	100.0%; Score 147; DB 2; Length 153;
KW	Cytokine; Glycoprotein; Growth factor; Immune response; Signal;	Best Local Similarity	100.0%; Pred. No. 5.2e-14;
KW	T-cell; -	Matches	30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT	SIGNAL 1 20 By similarity.	Qy	1 APTSSSTKTKTQLQLEHLLDLQMINLINGINN 30
FT	CHAIN 21 153 Interleukin-2.	Db	21 APTSSSTKTKTQLQLEHLLDLQMINLINGINN 50
FT	CARBHYD 23 23 O-linked (GalNAc. . .) (By similarity).		
FT	DISULFID 78 125 By similarity.		
SEQ	SEQUENCE 153 AA; 17628 MW; 59E240F25860F84 CRC64;		
<hr/>			
RESULT 5			
ID	IL2_MACFA	STANDARD;	PRT; 154 AA.
AC	ID_ IL2_MACFA		
DT	Q296515;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DB	Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGP) .		
GN	Name=IL2;		
OS	Macaca fasciularis (Crab eating macaque) (Cynomolgus monkey).		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
OC	Cercopithecinae; Macaca;		
OX	NCBI_TAXID=9541;		
RN	SEQUENCE FROM N.A.		
RC	TISSUE=Peripheral blood;		
RA	Yabe M.; Matsubara Y.; Tatsumi M.;		
RA	Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.		
RL	-1- FUNCTION: Produced by T-cells in response to antigenic or		
CC	mitogenic stimulation, this protein is required for T-cell		
CC	proliferation and other activities crucial to regulation of the		
CC	immune response. Can stimulate B cells, monocytes, lymphokine-		
CC	activated killer cells, natural killer cells, and glioma cells (By		
CC	similarity).		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- SIMILARITY: Belongs to the IL-2 family.		
<hr/>			
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entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).			
<hr/>			
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PCR rescued clones;		
RA	MEDLINE=22388257; PubMed=1477932; DOI=10.1073/pnas.242603899;		
RA	Klauser R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.P., Bhat N.K.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Tobiishi S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schniech A., Schein J.B.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences.";		
RD	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	SEQUENCE FROM N.A.		
RC	TISSUE=PCR rescued clones;		
RA	Strausberg R.;		
RA	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.		
EMBL; BC066254; AAH62254.1; -.	DR	GO: GO:0005176; C: extracellular; IEA.	
DR	GO: GO:0005134; F: interleukin-2 receptor binding; IEA.		
DR	GO: GO:0006955; P: immune response; IEA.		
DR	InterPro; IPR009079; 4 helix_cytokine.		
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RP	SEQUENCE FROM N.A.		
RC	TISSUE=PCR rescued clones;		
RA	Strausberg R.;		
RA	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.		
EMBL; BC066254; AAH62254.1; -.	DR	GO: GO:0005176; C: extracellular; IEA.	
DR	GO: GO:0005134; F: interleukin-2 receptor binding; IEA.		
DR	GO: GO:0006955; P: immune response; IEA.		
DR	InterPro; IPR009079; 4 helix_cytokine.		

OC Cercopithecinae; Papio.
 OX [1]
 RP SEQUENCE FROM N.A.
 RA Villinger F.;
 RT "Nonhuman primate cytokines."
 RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
 CC -1- FUNCTION: Produced by T-cells in response to antigenic or
 CC mitogenic stimulation, this protein is required for T-cell
 CC proliferation and other activities crucial to regulation of the
 CC immune response. Can stimulate B cells, monocytes, lymphokine-
 CC activated killer cells, natural killer cells, and glioma cells (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-2 family.
 CC
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 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AY234220; AAO85333.1; -.
 DR HSSP; P01585; IM49.
 DR InterPro; IPR003079; 4 helix Cytokine.
 DR InterPro; IPR000779; Interleukin-2.
 DR Pfam; PF00715; IL2; 1.
 DR PRINTS; PRO0265; INTERLEUKIN2.
 DR PRODOM; PD003649; Interleukin-2; 1.
 DR SMART; SM00189; IL2; 1.
 DR PROSITE; PS00424; INTERLEUKIN 2; 1.
 DR Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
 KW T-cell.
 FT SIGNAL 1 20 By similarity.
 FT CHAIN 21 154 Interleukin-2.
 FT DISULFID 78 126 By similarity.
 FT CARBOHYD 23 23 O-linked (GalNAC. . .) (By similarity).
 SQ SEQUENCE 154 AA; 17713 MW; 47F486BDF204AD6E CRC64;
 FT SIGNAL 1 20 By similarity.
 FT CHAIN 21 154 Interleukin-2.
 FT DISULFID 78 126 By similarity.
 FT CARBOHYD 23 23 O-linked (GalNAC. . .) (By similarity).
 SQ SEQUENCE 154 AA; 17713 MW; 47F486BDF204AD6E CRC64;

Query Match 100.0%; Score 147; DB 1; Length 154;
 Best Local Similarity 100.0%; Pred. No. 5.2e-14;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTSSSTKTKTQLEHILLDQMLINGINN 30
 Db 21 APTSSSTKTKTQLEHILLDQMLINGINN 50

RESULT 9
 IL2_SAISC STANDARD; PRT; 154 AA.
 ID IL2_SAISC
 AC Q8MKH2;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DB Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
 GN Saimiri sciureus (Common squirrel monkey).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buteraria; Primates; Platyrrhini; Cebidae; Saimiri.
 OX NCBI_TAXID=9521;
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21172722; PubMed=11976788; DOI=10.1007/s00251-002-0443-y;
 RX Heraud J.M.; Lavergne A.; Kazanji M.;
 RT "Molecular cloning, characterization, and quantification of squirrel
 monkey (Saimiri sciureus) Th1 and Th2 cytokines."
 RT Immunogenetics 54:20-29 (2002).
 CC -1- FUNCTION: Produced by T-cells in response to antigenic or
 CC mitogenic stimulation, this protein is required for T-cell
 CC proliferation and other activities crucial to regulation of the

CC immune response. Can stimulate B cells, monocytes, lymphokine-
 activated killer cells, natural killer cells, and glioma cells (By
 similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-2 family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF24755; AAR92042.1; -.
 DR HSSP; P01585; IM49.
 DR InterPro; IPR003079; 4 helix cytokine.
 DR InterPro; IPR000779; Interleukin-2.
 DR Pfam; PF00715; IL2; 1.
 DR PRINTS; PRO0265; INTERLEUKIN2.
 DR PRODOM; PD003649; Interleukin-2; 1.
 DR SMART; SM00189; IL2; 1.
 DR PROSITE; PS00424; INTERLEUKIN 2; 1.
 DR Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
 KW T-cell.
 FT SIGNAL 1 20 By similarity.
 FT CHAIN 21 154 Interleukin-2.
 FT DISULFID 78 126 By similarity.
 FT CARBOHYD 23 23 O-linked (GalNAC. . .) (By similarity).
 SQ SEQUENCE 154 AA; 17657 MW; AA642BABBCA87569 CRC64;
 Query Match 98.6%; Score 145; DB 1; Length 154;
 Best Local Similarity 96.7%; Pred. No. 1e-13;
 Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTSSSTKTKTQLEHILLDQMLINGINN 30
 Db 21 APTSSSTKTKTQLEHILLDQMLINGINN 50

RESULT 10
 O7JFM2 PRELIMINARY; PRT; 154 AA.
 ID O7JFM2
 AC Q7JFM2
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE IL-2.
 OS Aotus lemurinus (Northern gray-necked night monkey).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Primates; Primates; Platyrrhini; Cebidae; Actinidae; Aotus.
 OX NCBI_TAXID=43147;
 RN SEQUENCE FROM N.A.
 RP [1]
 RA Muriel L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
 RA Patarroyo M.E.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U88364; AAD41534.1; -.
 DR GO; GO:0005576; C:extracellular; DR GO; GO:0005134; F:Interleukin-2 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR00779; Interleukin-2.
 DR Pfam; PF00715; IL2; 1.
 DR PRINTS; PR00265; INTERLEUKIN2.
 DR PRODOM; PD003649; Interleukin-2; 1.
 DR SMART; SM00189; IL2; 1.
 DR PROSITE; PS00424; INTERLEUKIN 2; 1.
 DR SEQUENCE 154 AA; 17657 MW; AB52ABBADA96469 CRC64;
 Query Match 98.6%; Score 145; DB 2; Length 154;
 Best Local Similarity 96.7%; Pred. No. 1e-13;
 Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 11	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 13	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 14	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 15	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 16	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 17	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 18	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 19	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 20	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 21	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 22	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 23	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 24	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 25	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 26	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 27	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 28	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 29	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 30	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 31	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 32	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 33	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 34	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 35	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 36	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 37	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 38	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 39	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 40	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 41	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 42	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 43	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 44	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 45	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 46	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 47	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 48	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 49	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50
Qy	1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50	RESULT 50	Qy 1 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 30 Db 21 APTSSSTKTKTQLOLEHLLLDLQMLINGINN 50

DR InterPro; IPR005079; 4 helix cytokine.

DR InterPro; IPR005079; Interleukin-2 receptor binding; IEA.

DR PRINTS; PF00715; IL2; 1.

DR PRINTS; PRO00265; INTERLEUKIN2.

DR ProDom; PD003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

DR PROSITE; PS00424; INTERLEUKIN 2; 1.

DR SEQUENCE; 154 AA; 17675 MW; AB752ABBADA96469 CRC64;

Query Match Score 98.6%; Score 145; DB 2; Length 154;

Best Local Similarity 96.7%; Pred. No. 1e-13; Indels 0; Gaps 0;

Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APTSSSTKTKTQLEHLLDQMLINGINN 30

Db 21 APTSSSTKTKTQLEHLLDQMLINGINN 50

RESULT 15

Q6QWN0 PRELIMINARY; PRT; 133 AA.

ID Q6QWN0

AC Q6QWN0;

DT 05-JUL-2004 (T=EMBLrel. 27, Created)

DT 05-JUL-2004 (T=EMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (T=EMBLrel. 27, Last annotation update)

DB Interleukin-2.

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1]

RN _TAXID=9606;

SEQUENCE FROM N.A.

RA Submitted (JAN 2004) to the EMBL/GenBank/DBJ databases.

RA EMBL: AY2303040; ARS17753; 1; -

DR GO:0005576; C:extracellular; IEA.

DR GO: GO:0005134; F:interleukin-2 receptor binding; IEA.

DR GO: GO:0006955; P:immune response; IEA.

DR InterPro; IPR005079; 4 helix cytokine.

DR Pfam; PF00715; IL2; 1.

DR PRINTS; PRO0265; INTERLEUKIN 2.

DR ProDom; PD003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

DR PROSITE; PS00424; INTERLEUKIN 2; 1.

DR SEQUENCE; 133 AA; 15462 MW; 1699F680A09DB3B0 CRC64;

Query Match Score 97.3%; Score 143; DB 2; Length 133;

Best Local Similarity 100.0%; Pred. No. 1.8e-13; Indels 0; Gaps 0;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PTSSSTKTKTQLEHLLDQMLINGINN 30

Db 2 PTSSSTKTKTQLEHLLDQMLINGINN 30

RESULT 16

Q7Z7W3 PRELIMINARY; PRT; 133 AA.

ID Q7Z7W3

AC Q7Z7W3;

DT 01-OCT-2003 (T=EMBLrel. 25, Created)

DT 01-OCT-2003 (T=EMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (T=EMBLrel. 26, Last annotation update)

DB Interleukin-2.

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1]

RN _TAXID=9606;

SEQUENCE FROM N.A.

RA Chikara S. K., Jaiswal P., Sharma G.; Submitted (APR 2003) to the EMBL/GenBank/DBJ databases.

RA EMBL: AY283686; AAP5033-1; -

DR HSSP; P01505; 1M47.

DR InterPro; IPR005079; 4 helix cytokine.

DR Pfam; PF00715; IL2; 1.

DR PRINTS; PRO0265; INTERLEUKIN2.

DR ProDom; PD003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

DR PROSITE; PS00424; INTERLEUKIN 2; 1.

DR Cytokine; Glycoprotein; Growth factor; Immune response; Signal; T-cell.

RN T-cell.

RP SIGNAL; 1 20

RA By similarity.

RA Interleukin-2.

OC O-Linked (GalNAc . . .) (By similarity).

OC CARBOXYD; 23 23

OC CHAIN; 21 21

PT	DISULPID	78	126	By similarity.				
PT	VARIANT	25	25	R > S.				
PT	VARIANT	74	74	K -> E.				
SQ	SEQUENCE	154 AA;	17754 MW;	9FB851814204BA48	CRC64;			
Query Match	Best Local Similarity	96.5%	Score	142;	DB 1;	Length	154;	
Matches	29;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps 0;
Qy	1	APTSSTKTKTQLQLEHLLDQMLINGINN 30						
Db	21	APTSSTKTKTQLQLEHLLDQMLINGINN 50						
RESULT 18								
Q6NZ91		PRELIMINARY;		PRT;	153 AA.			
ID	Q6NZ91							
AC	Q6NZ91_							
DT	05-JUL-2004	(TREMBlrel. 27, Created)						
DT	05-JUL-2004	(TREMBlrel. 27, Last sequence update)						
DT	05-JUL-2004	(TREMBlrel. 27, Last annotation update)						
DE	Interleukin 2.							
OS	Homo sapiens (Human).							
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
NCBI_TaxID	9606;							
[1]								
SEQUENCE FROM N.A.								
Q6NZ91								
AC	Q6NZ91_							
DT	05-JUL-2004	(TREMBlrel. 27, Last sequence update)						
DE	Interleukin 2.							
OS	Homo sapiens (Human).							
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
NCBI_TaxID	9606;							
RN								
RP	SEQUENCE FROM N.A.							
TISSUE-PCR Rescued clones;								
RX	MEDLINE=2388257; PubMed=12477932; DOI=10.1101/phas.242603899;							
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Colling F.S., Wagner L., Shammam C.M., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diarchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udin T.B., Toshiyuki S., Carminci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalain D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahay J., Heitton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.J., Stalska U., Smalius D.E., Schein J.E., Jones S.J., Marrs M.A.; Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";							
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).							
RN	[2]							
RP	SEQUENCE FROM N.A.							
RA	Strausberg R.							
RA	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.							
DR	EMBL; BCO66256; AAH66256_1; -.							
DR	GO; GO:0005576; C:extracellular; IBA.							
DR	GO; GO:0005134; F:interleukin-2 receptor binding; IBA.							
DR	GO; GO:0006955; P:immune response; IBA.							
DR	InterPro; IPR009079; 4 helix cytokine.							
DR	InterPro; IPR00779; Interleukin-2.							
DR	PRINTS; PRO0265; INTERLEUKIN2.							
DR	PRODOM; PD003649; Interleukin-2; 1.							
DR	SMART; SM00189; IL2; 1.							
DR	PROSITE; PS00424; INTERLEUKIN-2; 1.							
DR	SEQUENCE 156 AA; 18002 MW; 8B045D43B3J6389 CRC64;							
Qy	Query Match							
Db	Best Local Similarity	92.2%	Score	135.5;	DB 2;	Length	156;	
Matches	30;	Conservative	0;	Mismatches	0;	Indels	3;	Gaps 0;
Qy	1	APTSSS-TKTKTQLQLEHLLDQMLINGINN 30						
Db	21	APTSSTKTKTQLQLEHLLDQMLINGINN 53						
RESULT 20								
Q16334		PRELIMINARY;		PRT;	139 AA.			
ID	Q16334							
AC	Q16334_							
DT	01-NOV-1996 (TREMBlrel. 01, Created)							
DT	01-NOV-1996 (TREMBlrel. 01, Last sequence update)							
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)							
DE	IL-2 protein (Fragment).							
GN	Name=IL-2;							
OS	Homo sapiens (Human).							
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
NCBI_TaxID	9606;							
[1]								
SEQUENCE FROM N.A.								
RA	Query Match							
RA	Best Local Similarity	93.2%	Score	137;	DB 2;	Length	153;	
RA	Matches	29;	Conservative	0;	Mismatches	1;	Indels	0;
RA	Qy	1	APTSSS-TKTKTQLQLEHLLDQMLINGINN 30					
RA	Db	21	APTSSTKTKTQLQLEHLLDQMLINGINN 53					

DR	PROSITE: PS00424; INTERLEUKIN 2;
RA	Cytokine; Glycoprotein; Growth Factor; Immune response; Signal;
RA	KW T-cell.
RT	Interleukin-2 transcripts in human and rodent brains: possible expression by astrocytes.;
RT	J. Neurochem. 64:1938-1936(1995).
RL	DR EMBL; S7735; ADD14564.1; -.
RL	DR HSSP; P60568; 1IRL.
DR	GO: GO:0005576; C: extracellular; IEA.
DR	GO; GO:0005134; P: immune response; IEA.
DR	GO; GO:006955; P: helix cytokine.
DR	InterPro; IPR009079; 4-helix cytokine.
DR	InterPro; IPR00779; Interleukin-2.
DR	DR Pfam; PF00715; IL2; 1.
DR	PRINTS; PR00265; INTERLEUKIN2
DR	ProDom; P003659; Interleukin-2; 1.
DR	SMART; SM00189; IL2; 1.
DR	PROSITE; PS00424; INTERLEUKIN_2; 1.
FT	NON-TER 139 139 AA; 15986 MW; 731PBA40D0C63C5 CRC64;
SQ	SEQUENCE 139 AA; 15986 MW; 731PBA40D0C63C5 CRC64;
	RESULT 22
	IL2_FELCA
	ID IL2_FELCA STANDARD; PRT; 154 AA.
	AC 007885;
	DT 01-OCT-1994 (Rel. 30, Created)
	DR 01-OCT-1994 (Rel. 30, Last sequence update)
	DR 05-JUN-2004 (Rel. 44, Last annotation update)
	DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
	GN Name=IL2;
	OS Felis silvestris catus (Cat).
	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
	OC NCBI_TAXID=9685;
	RN [1]
	SEQUENCE FROM N.A.
	RP MEDLINE=933556765; PubMed=8352761;
	RA Cozzi P.J.; Padrid P.A.; Takeda J.; Alegre M.-A.; Yuhki N.; Leff A.R.;
	RT <i>Sequence and functional characterization of feline interleukin 2.</i> ;
	RL Biochem. Biophys. Res. Commun. 194:1038-1043 (1993).
	RN [2]
	SEQUENCE FROM N.A.
	RA Litman R.; Gibbs C.; Good R.A.; Day N.K.;
	RL Submitted' (NOV-1994) to the EMBL/GenBank/DBJ databases.
	CC -1- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.
	CC -1- SUBCELLULAR LOCATION: Secreted.
	CC -1- SIMILARITY: Belongs to the IL-2 family.
	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
	CC or send an email to license@isb-sib.ch).
	CC DR EMBL; L19402; AA02865.1; -.
	CC DR EMBL; L25408; AA51431.1; -.
	CC DR PIR; JN698; JN698.
	CC CC HSSP; P01505; IM49.
	CC CC InterPro; IPR000079; 4-helix cytokine.
	CC CC InterPro; IPR000779; Interleukin-2.
	CC CC Pfam; PF00715; IL2; 1.
	CC CC PRINTS; PR00265; INTERLEUKIN2.
	CC CC DR SMART; SM00189; IL2; 1.
	CC CC DR PROSITE; PS00424; INTERLEUKIN 2;
	CC CC KW Cytokine; Glycoprotein; Growth Factor; Immune response; Signal;
	CC CC FT SIGNAL; 21 154
	CC CC FT DISULFID 78 126
	CC CC FT SIGNAL; 21 154
	CC CC FT DISULFID 78 126

PT	CARBOHYD	111	111	4	N-linked (GlcNAc, ·) (Potential).	RL	Submitted (JAN-2001) to the EMBL/GenBank/DBBJ databases.
PT	CONFLICT	3	4	·	KI -> RM (in Ref. 2).	DR	EMBL; AF332117; AAK01437.1; -.
PT	CONFLICT	150	150	·	F -> I (in Ref. 2).	DR	HSSP; P6058; 1IRL.
SQ	SEQUENCE	154	AA;	17653	MW; 2E71EEBD8B96658EP CRC64;	DR	GO; GO:0005576; C:extracellular; IEA.
Query Match	Score 114;	DB 1;	Length 154;			DR	GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
Best Local Similarity	77.6%	Pred. No. 5.2e-05;				DR	GO; GO:0005955; P:immune response; IEA.
Matches	22;	Conservative	5;	Mismatches	3;	DR	InterPro; IPR009079; 4 helix cytokine.
Qy	1	APSSSTKTKTQLEHLLDLQMLNLGNNN	30			DR	InterPro; IPR000779; Interleukin-2.
Db	21	APASSSTKETQQQLEQQLLDRLLNGVNN	50			DR	Pfam; PF00715; IL2; 1.
						DR	PRINTS; PRO0265; INTERLEUKIN2.
						DR	ProDom; PD003649; Interleukin-2; 1.
						DR	SMART; SM00189; IL2; 1.
						FT	NON-TER 1
						FT	NON-TER 66
						FT	66
					SQ	SEQUENCE 66 AA; 7389 MW; 22A893F79DA2AE47 CRC64;	
RESULT 23							
Q9XT83	PRELIMINARY;		PRT;	155 AA.	Query	Match 73.1%; Score 107.5;	DB 2;
AC					Best Local Similarity 71.0%;	Pred. No. 1.9e-08;	
DT	01-NOV-1999	(TREMBLrel.	12;	Created)	Matches 22;	Mismatches 6;	
DT	01-MAR-2004	(TREMBLrel.	12;	Last sequence update)	Conservative	2;	
DT	01-MAR-2004	(TREMBLrel.	26;	Last annotation update)	Indels 1;	Gap 1;	
DE							
OS	Halichoerus grypus	(Gray seal).					
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;						
OC	Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Halichoeridae.						
OX	NCBI_TaxID=9711;						
RN							
RP	SEQUENCE FROM N.A.						
RN	MEDLINE=99221046.	PubMed=10206205;	DOI=10.1016/S0165-2427(99)00009-4;				
RA	St-Laurent G., Beliveau C., Archambault D.;						
RT	"Molecular cloning and phylogenetic analysis of beluga whale						
RT	(Delphinapterus leucas) and grey seal (Halichoerurus Grypus) interleukin						
RT	2.;"						
RL	Vet. Immunol. Immunopathol.	67:385-394 (1999).					
DR	EMBL; AF028781; P4D40848.1; -.						
DR	HSSP; P6058; 1IRL.						
DR	GO; GO:0005376; C:extracellular; IEA.						
DR	GO; GO:0005134; F:interleukin-2 receptor binding; IEA.						
DR	GO; GO:0006555; F:immune response; IEA.						
DR	InterPro; IPR009079; 4 helix cytokine.						
DR	InterPro; IPR000779; Interleukin-2.						
DR	Pfam; PF00715; IL2; 1.						
DR	PRINTS; PRO0265; INTERLEUKIN2.						
DR	ProDom; PD003649; Interleukin-2; 1.						
DR	SMART; SM00189; IL2; 1.						
DR	PROSITE; PS00424; INTERLEUKIN-2;						
SQ	SEQUENCE 155 AA; 17860 MW; P18P449AC672241A CRC64;						
Query Match	Score 73.8%;	DB 2;	Length 155;				
Best Local Similarity	74.2%;	Pred. No. 3.6e-08;					
Matches	23;	Conservative	5;	Mismatches	2;		
Qy	1	AP-TSSSTKTKTQLEHLLDLQMLNLGNNN	30				
Db	21	APTTSSSTKETQQQLEQQLLDRLLNGVNN	51				
RESULT 24							
Q9BG74	PRELIMINARY;		PRT;	66 AA.	Query	Match 70.5%; Score 106.5;	DB 2;
AC	Q9BG74;				Best Local Similarity 69.0%;	Pred. No. 1.9e-08;	
DT	01-JUN-2001	(TREMBLrel.	17;	Created)	Matches 22;	Mismatches 6;	
DT	01-MAR-2004	(TREMBLrel.	17;	Last sequence update)	Conservative	2;	
DE	Interleukin 2 (Fragment).				Indels 1;	Gap 1;	
OS	Canis familiaris (Dog).						
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;						
OC	Mammalia; Eutheria; Carnivora; Pinnipedia; Canidae.						
OX	NCBI_TaxID=9615;						
RN	SEQUENCE FROM N.A.						
RC	SEQUENCE FROM N.A.						
RN	SEQUENCE FROM N.A.						
RC	SEQUENCE FROM N.A.						
RA	MEDLINE=96016636; PubMed=8571541; DOI=10.1016/0165-2427(94)05400-M;						
RA	Somberg R.L., Pullen R.P., Casal M.L., Patterson D.F., Felsburg P.J.,						
RA	Henthorn P.S.;						
RA	"A single nucleotide insertion in the canine interleukin-2 receptor						
RA	gamma chain results in X-linked severe combined immunodeficiency						
RA	disease.";						
RA	RT						
RA	RT						
RA	RT						
RA	RT						
RA	RT						
RN	SEQUENCE FROM N.A.						
RC	SEQUENCE FROM N.A.						
RX	MEDLINE=93347614; PubMed=7622066; DOI=10.1016/0378-1119(95)00078-K;						
RA	Knapp D.W., Williams J.S., Andrianan O.M.;						
RT	"Cloning of the canine interleukin-2-encoding cDNA."						
RL	Gene 159:281-292 (1995).						
CC	-I- FUNCTION: Produced by T-cells in response to antigenic or						
CC	mitogenic stimulation, this protein is required for T-cell						
CC	proliferation and other activities crucial to regulation of the						
CC	immune response. Canine T cells, monocytes, lymphokine-						
CC	activated killer cells, natural killer cells, and glioma cells.						
CC	-I- SUBCELLULAR LOCATION: Secreted.						
CC	-I- SIMILARITY: Belongs to the IL-2 family.						
CC	-I- This SWISS-PROT entry is copyright. It is produced through a collaboration						
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation-						
CC	the European Bioinformatics Institute. There are no restrictions on its						
CC	use by non-profit institutions as long as its content is in no way						

CC	immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.	Query Match	72.1%; Score 106; DB 2; Length 133;
CC	- - SURCELLULAR LOCATION: secreted.	Best Local Similarity	72.4%; Pred. No. 7.2e-08;
CC	- - SIMILARITY: Belongs to the IL-2 family.	Matches	21; Mismatches 5; Indels 0; Gaps 0;
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	Qy	1 APTSSSTKTKTQQLQLEHLLDQMLINGIN 29
CC	EMBL; AF068057; AAC23838_1; -.	Db	21 APTSSSTKETQQLDQMLDQVLKGVN 49
DR	DR; HSSP; P01585; 1MAA.	RESULT 30	0923T2
DR	DR; InterPro; IPR009079; 4_helix_cytokine.	ID	0923T2
DR	DR; InterPro; IPR000779; Interleukin-2.	AC	0923T2; PRELIMINARY;
DR	DR; Pfam; PF00715; IL2; 1.	DT	01-DEC-2001 (TREMBLrel. 19; Created)
DR	DR; PRINTS; PRO0265; INTERLEUKIN2.	DT	01-MAR-2004 (TREMBLrel. 19; Last sequence update)
DR	DR; SMART; SM003649; Interleukin-2; 1.	DB	DB; Interleukin 2.
DR	DR; SMART; SM00389; Interleukin-2; 1.	OS	Sigmodon hispidus (Hispid cotton rat).
DR	DR; PROSITE; PS00424; INTERLEUKIN 2; 1.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
KW	KW; Cytokine; Glycoprotein; Growth factor; Immune response; Signal; T-cell.	OC	Sigmodon
FT	FT SIGNAL 1 20 By similarity.	OC	NCBI_TaxID=42415;
FT	FT CHAIN 21 153 Interleukin-2.	RN	SEQUENCE FROM N.A.
FT	FT CARBOHYD 23 23 O-linked (GALNAC. . .) (By similarity).	RA	Darnell M.R., Pleiteeva L.M., Langley R.J., Blanco J.C., Prince G.A.;
FT	FT CARBOHYD 111 111 N-linked (GICNAC. . .) (Potential).	RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
FT	FT DISULFID 78 125 By similarity.	DR	EMBL; AF398549; AAC94012.1; -.
SQ	SQ DISULFID 153 AA; 17256 MW; 817353 6B2DD8BB86 CRC64;	DR	HSSP; P60568; 1RL.
DR	DR; Sequence Match 72.8%; Score 107; DB 1; Length 153; Best Local Similarity 70.0%; Pred. No. 5.9e-08; Gaps 0; Matches 21; Conservative 6; Mismatches 3; Indels 0; Gaps 0;	DR	C:extracellular; IEA.
DR	DR; Q9MZR9 PRELIMINARY; PRT; 133 AA.	DR	GO; GO:0005134; P:interleukin-2 receptor binding; IEA.
DR	DR; Q9MZR9 ID 01-OCT-2000 (TREMBLrel. 15; Created)	DR	GO; GO:000955; P:immune response; IEA.
DR	DR; Q9MZR9 DT 01-OCT-2000 (TREMBLrel. 15; Last sequence update)	DR	Pfam; PF00715; IL2; 1.
DR	DR; Q9MZR9 DT 01-MAR-2004 (TREMBLrel. 26; Last annotation update)	DR	PRINTS; PR00265; INTERLEUKIN-2; 1.
DR	DR; Q9MZR9 DE Interleukin 2 variant IL2delta2.	DR	SMART; SM00189; IL2; 1.
GN	GN; Name=IL-2;	DR	PROSITE; PS00424; INTERLEUKIN_2; 1.
OS	OS Oryctolagus cuniculus (Rabbit); Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	DR	SEQUENCE FROM N.A.
OC	OC	Db	155 AA; 17627 MW; ACDAEA865B993291 CRC64;
OX	OX	RESULT 31	070329
RN	RN; Q9MZR9 PRELIMINARY; PRT; 133 AA.	ID	070329
DR	DR; Sequence Match 72.1%; Score 106; DB 2; Length 155; Best Local Similarity 73.3%; Pred. No. 8.6e-08; Matches 22; Conservative 3; Mismatches 5; Indels 0; Gaps 0;	AC	SEQUENCE FROM N.A.
DR	DR; Q9MZR9 ID 01-OCT-2000 (TREMBLrel. 15; Created)	AC	070329; TISSUE=Spleen;
DR	DR; Q9MZR9 DT 01-OCT-2000 (TREMBLrel. 15; Last sequence update)	DT	01-AUG-1998 (TREMBLrel. 07; Created)
DR	DR; Q9MZR9 DT 01-MAR-2004 (TREMBLrel. 26; Last annotation update)	DT	01-AUG-1998 (TREMBLrel. 07; Last sequence update)
DR	DR; Q9MZR9 DE Interleukin-2 (Fragment)	DT	01-MAR-2004 (TREMBLrel. 26; Last annotation update)
DR	DR; Q9MZR9 OS Mesocricetus auratus (Golden hamster).	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
DR	DR; Q9MZR9 RN NCBI_TaxID=10036;	OX	NCBI_TaxID=10036;
DR	DR; Q9MZR9 RN NCBI_TaxID=9986;	RN	SEQUENCE FROM N.A.
DR	DR; Q9MZR9 RN NCBI_TaxID=9986; TISSUE=Spleen;	RC	TISSUE=Spleen;
DR	DR; Q9MZR9 RN NCBI_TaxID=9986; MEDLINE=95234044; PubMed=9573100;	RX	MEDLINE=95234044; PubMed=9573100;
DR	DR; Q9MZR9 RN NCBI_TaxID=9986; Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.,	RA	Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.,
DR	DR; Q9MZR9 RN NCBI_TaxID=9986; "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and analysis of cytokine mRNA expression in experimental visceral leishmaniasis".	RT	"Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and analysis of cytokine mRNA expression in experimental visceral leishmaniasis".
DR	DR; Q9MZR9 RN NCBI_TaxID=9986; Infect Immun 66:2135-2142 (1998).	RL	Infect Immun 66:2135-2142 (1998).
DR	DR; Q9MZR9 RN NCBI_TaxID=9986; AAC0097.1; -.	DR	AAC0097.1; -.
DR	DR; Q9MZR9 RN NCBI_TaxID=9986; P60568; 1RL.	DR	HSSP; P60568; 1RL.
DR	DR; Q9MZR9 RN NCBI_TaxID=9986; GO; GO:0005576; C:extracellular; IEA.	DR	GO; GO:0005576; C:extracellular; IEA.
DR	DR; Q9MZR9 RN NCBI_TaxID=9986; GO; GO:0005134; P:interleukin-2 receptor binding; IEA.	DR	GO; GO:0005134; P:interleukin-2 receptor binding; IEA.
DR	DR; Q9MZR9 RN NCBI_TaxID=9986; GO; GO:0006555; P:immune response; IEA.	DR	GO; GO:0006555; P:immune response; IEA.
DR	DR; Q9MZR9 RN NCBI_TaxID=9986; InterPro; IPR009079; 4_helix_cytokine.	DR	InterPro; IPR009079; 4_helix_cytokine.
DR	DR; Q9MZR9 RN NCBI_TaxID=9986; ProDom; PF00175; IL2; 1.	DR	ProDom; PF00175; IL2; 1.
DR	DR; Q9MZR9 RN NCBI_TaxID=9986; SMART; SM00189; IL2; 1.	DR	SMART; SM00189; IL2; 1.
DR	DR; Q9MZR9 RN NCBI_TaxID=9986; SEQUENCE 133 AA; 14748 MW; 0D54758C190B5655 CRC64;	DR	SEQUENCE 133 AA; 14748 MW; 0D54758C190B5655 CRC64;

GO; GO:0005134; P:interleukin-2 receptor binding; IBA.
 DR GO:0006955; B:immune response; IBA.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR000779; Interleukin-2.
 DR PRINTS; PRO0265; INTERLEUKIN2.
 DR Prodrom; P003649; Interleukin-2; 1.
 DR PROSITE; SM00189; IL2; 1.
 DR PROSITE; PS00424; INTERLEUKIN_2; 1.
 FT NON-TER 1 138 AA; 15739 MW; 351032995B670779 CRC64;
 SQ SEQUENCE 138 AA; 15739 MW; 351032995B670779 CRC64;

Query Match Score 70.1%; Best Local Similarity 73.3%; Score 103; Best Local Similarity 73.3%; Pred. No. 2, 1e-07; Length 138; Matches 22; Conservative 2; Mismatches 6; Indels 0; Gaps 0; RBSULT 33

Qy 1 APTSSSTKTKTQLEHLLDQMLNGINN 30
 Db 14 APTSSSTKTKTQLEHLLDQMLNGINN 43

RESULT 32

IL2_RAT ID IL2_RAT STANDARD; PRT; 155 AA.
 AC P1108 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
 GN Name=IL2; Synonyms=IL-2;
 OS Rattus norvegicus (Rat).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
 OC NCBITaxonID=10116;
 RN [1] RP SEQUENCE FROM N.A.
 RXN MEDLINE=89339605; PubMed=2788130;
 RA McKnight, A.J., Mason, D.W., Barclay, A.N.;
 RT "Sequence of rat interleukin 2 and anomalous binding of a mouse
 RT interleukin 2 cDNA probe to rat MHC class II-associated invariant
 RT chain mRNA.",
 RL Immunogenetics 30:145-147(1989).
 CC -I- FUNCTION: Produced by T-cells in response to antigenic or
 CC mitogenic stimulation, this protein is required for T-cell
 CC proliferation and other activities crucial to regulation of the
 CC immune response. Can stimulate B cells, monocytes, lymphokine-
 CC activated killer cells, natural killer cells, and glioma cells.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- SIMILARITY: Belongs to the IL-2 family.
 CC

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DR EMBL; M22899; AAA41427.1; -.
 DR PIR; A45882; A31278.
 DR HSSP; P01585; IM49.
 DR RGD; 620047; IL2.
 DR InterPro; IPR000979; 4_helix_cytokine.
 DR InterPro; IPR000779; Interleukin-2.
 DR PRINTS; PRO0265; INTERLEUKIN2.
 DR Prodrom; P003649; Interleukin-2; 1.
 DR PROSITE; SM00189; IL2; 1.
 DR PROSITE; PS00424; INTERLEUKIN_2; 1.
 DR SMART; SM00189; IL2; 1.
 DR SMART; SM01189; IL2; 1.
 DR PROSITE; PS00424; INTERLEUKIN_2; 1.
 DR Cytokine; Glycoprotein; Growth factor; Immune response; Signal; T-cell.
 KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal; T-cell.
 KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal; T-cell.

FT SIGNAL 1 20 By similarity.

FT PT CHAIN 21 155 Interleukin-2.
 FT CARBOHYD 23 23 O-linked (GalNAc. . .) (By similarity).
 FT DISUFRID 78 126 By similarity.
 SQ SEQUENCE 155 AA; 17632 MW; 670A554A73BF30A0 CRC64;
 Query Match Score 97; DB 1; Length 155;
 Best Local Similarity 66.7%; Pred. No. 2e-06; Mismatches 4; Indels 0; Gaps 0;
 Matches 20; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 APTSSSTKTKTQLEHLLDQMLNGINN 30
 Db 21 APTSSPAKETQHLSQILLDQVLRGIDN 50

RESULT 34

IL2_PIG ID IL2_PIG STANDARD; PRT; 154 AA.
 AC P26791; DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DB Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
 GN Name=IL2;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1] OC Mammalia; Eutheria; NCBI_TaxID=9822;
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=91274360; PubMed=2054386; DOI=10.1016/0167-4781(91)90019-1;
 RX Goodall, J.C., Emery, D.C., Bailey, M., English, L.S., Hall, L.;
 RT "cDNA cloning of porcine interleukin 2 by polymerase chain reaction.",
 RL Biochim. Biophys. Acta 1089:257-258(1991).
 RN [2] RN RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RL Lefevre, F.;
 RL Submitted (MAY-1991) to the EMBL/GenBank/DBJ/GenBank databases.
 RN [3] RN RP SEQUENCE FROM N.A.
 RA Iwata, H., Hasegawa, A., Yamamoto, M., Oida, T., Endo, Y., Inoue, T.;
 RT "Structure of the porcine chromosomal interleukin-2 gene.";
 CC Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: Produced by T-cells in response to antigenic or
 CC mitogenic stimulation, this protein is required for T-cell
 CC proliferation and other activities crucial to regulation of the
 CC immune response. Can stimulate B cells, monocytes, lymphokine-
 CC activated killer cells, natural killer cells, and glioma cells.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- SIMILARITY: Belongs to the IL-2 family.
 CC

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CC DR EMBL; X56750; CAA40071.1; -.
 CC DR EMBL; X58428; CAA41330.1; -.
 CC DR PIR; S16241; S16241.
 CC DR HSSP; P01585; IM49.
 CC DR InterPro; IPR00079; 4_helix_cytokine.
 CC DR PRINTS; PRO00079; 4_helix_cytokine.
 CC DR InterPro; IPR000779; Interleukin-2.
 CC DR P00265; INTERLEUKIN2.
 CC DR PRODom; P003649; Interleukin-2; 1.
 CC DR SMART; SM00189; IL2; 1.
 CC DR SMART; SM01189; IL2; 1.
 CC DR PROSITE; PS00424; INTERLEUKIN_2; 1.
 CC KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal; T-cell.
 CC KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal; T-cell.

KW	T-cell.	1	20	By similarity.				
PT	SIGNAL	21	154	Interleukin-2.				
PT	CHAIN	21	23	O-linked (GALNAC. . .) (By similarity).				
PT	CARBOHYD	23	78	By similarity.				
PT	DISULFID	78	126	By similarity.				
SQ	SEQUENCE	154 AA;	17401 MW;	F3B9543D4A3D3E1 CRC64;				
Query Match	Best Local Similarity	65.3%	Score 96; DB 1; Length 154;					
Matches	20; Conservative	4;	Mismatches 6; Indels 0; Gaps 0;					
Qy	1 APSSSTKTKTQLEHLLDQMLNGINN 30							
Db	21 APSSSTKTKTQLEHLLDQMLKEVNN 50							
	RESULT 34							
II12-MBRN	ID II12-MERUN	STANDARD;	PRT;	155 AA.				
AC	Q08781;							
DR	01-OCT-1994 (Rel. 30, Created)							
DR	01-OCT-1994 (Rel. 30, Last sequence update)							
DR	05-JUL-2004 (Rel. 44, Last annotation update)							
DB	Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).							
GN	Name=IL2;							
OS	Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).							
OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;							
OC	NCBI_TaxID=10047;							
RN	RP:SEQUENCE FROM N.A.							
RC	TISSUE=Spleen;							
RX	MEDLINE=94174702; PubMed=8128610; DOI=10.1016/0165-2427(94)90015-9;							
RX	Mai Z., Kousoulas K.G., Horroh D.W., Klei T.R., Horroh D.W., Klei T.R.,							
RX	"Cross-species PCR cloning of gerbil (Meriones unguiculatus) interleukin-2 cDNA and its expression in COS-7 cells.";							
RT	interleukin-2							
RT	SMART: SM00189; IL2; 1.							
RT	PROSITE: PS00424; INTERLEUKIN-2; 1.							
CC	-1- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.							
CC	-1- SUBCELLULAR LOCATION: Secreted.							
CC	-1- SIMILARITY: Belongs to the IL-2 family.							
CC	-----							
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).							
CC	-----							
DR	X68779; CA048679.1; -.							
DR	PRIB: S33509; S33509.							
DR	DR PIR: S01585; IM9.							
DR	InterPro: IPR00979; 4 helix cytokine.							
DR	PRINTS: PR00079; IL2; 1.							
DR	PRODOM: P00265; INTERLEUKIN2.							
DR	SMART: SM00189; Interleukin-2; 1.							
DR	PROSITE: PS00424; Interleukin-2; 1.							
KW	Cytokine; Glycoprotein; Growth factor; Immune response; Signal;							
PT	CHAIN	1	20	By similarity.				
PT	CARBOHYD	21	155	Interleukin-2.				
PT	DISULFID	23	23	O-linked (GALNAC. . .) (By similarity).				
SQ	SEQUENCE	155 AA;	17602 MW;	D0P7AA1A81CDDA CRC64;				
Query Match	64.6%; Score 95; DB 1; Length 155;							

	Best Local Similarity	66.7%	Pred. No. 4e-06;					
	Matches	20;	Conservative	2;	Mismatches	8;	Indels	0; Gaps 0;
Qy	1 APSSSTKTKTQLEHLLDQMLNGINN 30							
Db	21 APSSSTKTKTQLEHLLDQMLKEVNN 50							
	RESULT 35							
	Q865X2	PRELIMINARY;	PRT;	154 AA.				
ID	Q865X2;							
AC	Q865X2;							
DR	01-JUN-2003 (TREMBLrel. 24, Created)							
DR	01-JUN-2003 (TREMBLrel. 24, Last sequence update)							
DR	01-MAR-2004 (TREMBLrel. 26, Last annotation update)							
DE	Interleukin 2.							
GN	Name=IL-2;							
OS	Lama glama (Llama).							
OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Tylopoda; Camelidae; Lama.							
RA	Raadon O., Lee S.-., Yoshida R., Chang K.-., Ohashi K., Sugimoto C., Onuma M.;							
RA	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.							
DR	EMBL: AB107651; BAC75388.1; -.							
DR	HSSP: P60568; 1IRL.							
DR	GO; GO:0005576; C:extracellular; IEA.							
DR	GO; GO:005134; F:interleukin-2 receptor binding; IEA.							
DR	GO; GO:006955; P:immune response; IEA.							
DR	InterPro; IPR00079; 4 helix cytokine.							
DR	InterPro; IPR00779; Interleukin-2.							
DR	PFam; PF00715; IL2; 1.							
DR	PRINTS; PR00365; INTERLEUKIN2.							
DR	PRODOM; PD003649; Interleukin-2; 1.							
DR	SMART; SM00189; IL2; 1.							
DR	PROSITE; PS00424; INTERLEUKIN-2; 1.							
SQ	SEQUENCE	154 AA;	17652 MW;	-8020BC8DD87BBA38 CRC64;				
	Query Match	63.3%	Score 93; DB 2; Length 154;					
	Best Local Similarity	66.7%	Pred. No. 7.9e-06;					
	Matches	20;	Conservative	3;	Mismatches	7;	Indels	0; Gaps 0;
Qy	1 APSSSTKTKTQLEHLLDQMLNGINN 30							
Db	21 APSSSTKTKTQLEHLLDQMLKEVNN 50							
	RESULT 36							
ID	IL2_HORSE STANDARD							
AC	P37597;							
DT	01-OCT-1994 (Rel. 30, Created)							
DR	01-NOV-1995 (Rel. 32, Last sequence update)							
DR	05-JUL-2004 (Rel. 44, Last annotation update)							
DR	Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).							
GN	Name=IL2;							
OS	Equus caballus (Horse).							
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Equidae; Equus.							
OC	Vandergrift E.V., Horroh D.W.;							
OC	"Molecular cloning and expression of equine interleukin 2."							
RN	RP:SEQUENCE FROM N.A.							
RX	MEDLINE=9116538; PubMed=8116217; DOI=10.1016/0165-2427(93)90070-K;							
RA	SEQUENCE FROM N.A.							
RA	Tavernor A.S., Allen W.R., Butcher G.W.;							
RL	Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.							
CC	-1- FUNCTION: Produced by T-cells in response to antigenic or							

CC	mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- SIMILARITY: Belongs to the IL-2 family.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
DR	EMBL; L06009; AAA20134.1; -.
DR	EMBL; X69193; CAA49190.1; -.
PIR	S31391; S31391.
HSSP	P01585; M147.
InterPro	IPIR009079; 4_helix_cytokine.
InterPro	IPIR000779; Interleukin-2.
Pfam	PF00715; IL2; 1.
PRINTS	PR00265; INTERLEUKIN2.
PRODOM	PD003649; Interleukin-2; 1.
SMART	SM00189; IL2; 1.
PROSITE	PS00424; INTERLEUKIN 2; 1.
Cytokine	Glycoprotein; Growth factor; Immune response; Signal; T-cell.
KW	
SIGNAL	1 20 By similarity.
FT	CHAIN 21 149 By similarity.
FT	DISULFID 78 121 By similarity.
PT	CARBOHYD 23 23 O-linked (GalNAc. . .) (By similarity).
PT	CARBOHYD 106 106 N-linked (GlcNAc. . .) (Potential).
CONFLICT	3 3 R -> K (in Ref. 2).
PT	CONFLICT 8 8 S -> A (in Ref. 2).
PT	CONFLICT 59 59 I -> M (in Ref. 2).
PT	CONFLICT 125 125 N -> D (in Ref. 2).
PT	CONFLICT 128 128 E -> G (in Ref. 2).
PT	CONFLICT 145 145 I -> P (in Ref. 2).
PT	CONFLICT 148 148 L -> M (in Ref. 2).
SEQUENCE	149 AA; 17086 MW; 051BB8C47A0114FC CRC64;
SQ	62.6% Score 92; DB 1; Length 149; Pred. No. 1.1e-05; Mismatches 17; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
Query Match	1 APTSSSTKTKTQLEHLLQMLNGINN 30
Db	21 APTSSSKRQQQLQMLKLLLEGVN 50
RESULT 37	
Q9UCF5	PRELIMINARY; PRT; 23 AA.
AC	Q9UCF5; PRELIMINARY; PRT; 23 AA.
01-MAY-2000	(TREMBLrel. 13, Created)
01-MAY-2000	(TREMBLrel. 13, Last sequence update)
01-JUN-2000	(TREMBLrel. 14, Last annotation update)
DE	Interleukin 2 (Fragment).
Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;	
[1]	SEQUENCE.
RP	MEDLINE=328963; PubMed=851072; DOI=10.1006/abio.1993.1209;
RX	Mullner S, Karbe-Rhonges B, Trippier D; "Charge heterogeneity of insulin fusion proteins expressed in Escherichia coli is not due to proteolytic degradation.";
PT	Anal. Biochem. 210:366-73 (1993).
SEQUENCE	23 AA; 2637 MW; 40B64C6875CE021F CRC64;
Query Match	59.9% Score 88; DB 1; Length 152; Best Local Similarity 60.0%; Pred. No. 4.5e-05; Mismatches 6; Indels 0; Gaps 0
Db	1 APTSSSTKTKTQLEHLLQMLNGINN 30
21 APTSSSKRQQQLQMLKLLLEGVN 50	

RESULT 39

Q71V48	PRELIMINARY;	PRT;	38 AA.
ID Q71V48			
AC			
DR 05-JUL-2004 (TREMBLrel. 27, Created)			
DR 05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DR Interleukin-2 (Fragment).			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominoidea; Homo.			
NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Turner D.M.; Sinnott P.J.; Hutchinson I.V.;			
RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.			
DR EMBL; AF031845; BAA86861.1;			
DR GO; GO:0005576; C:extracellular; IEA.			
DR GO; GO:005134; F:interleukin-2 receptor binding; IEA.			
DR GO; GO:0006955; P:immune response; IEA.			
DR InterPro; IPR000779; Interleukin-2.			
DR Pfam; PF00715; IL12; 1.			
DR ProDom; PD003649; Interleukin-2; 1.			
PT NON-TER	38		
SEQUENCE 38 AA;	4192 MW;	8DE4AE5344C2CBA3 CRC64;	

Query Match 59.2%; Score 87; DB 2; Length 38;

Best Local Similarity 100.0%;	Pred. No. 1.3e-05;	Indels 0;	Gaps 0;
Matches 18; Conservative 0;	Mismatches 0;		
Db 21 APPSSSTKTKTQLEHLI 18			
RN 21 APPSSSTKTKTQLEHLI 38			

Qy 1 APPSSSTKTKTQLEHLI 18

Db 21 APPSSSTKTKTQLEHLI 38

RESULT 40

Q9XTB4	PRELIMINARY;	PRT;	154 AA.
ID Q9XTB4			
AC			
DR 01-NOV-1999 (TREMBLrel. 12, Created)			
DR 01-MAR-2004 (TREMBLrel. 12, Last sequence update)			
DR Interleukin 2.			
OS Delphinapterus leucas (Beluga whale).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Monodontidae; Delphinapterus.			
NCBI_TaxID=9749;			
RN [1]			
RP SEQUENCE FROM N.A.			
RR MEDLINE=99221046; PubMed=10206205; DOI=10.1016/S0165-2427(99)00009-4;			
RA St-Laurent G.; Beliveau C.; Archambault D.;			
RT "Molecular cloning and phylogenetic analysis of beluga whale (Delphinapterus leucas) and grey seal (Halichoerus grypus) interleukin 2."			
RT InterPro; IPR000779; Interleukin-2.			
RT InterPro; IPR000779; IL12; 1.			
DR Pfam; PF00715; IL12; 1.			
DR PRINTS; PRO0265; INTERLEUKIN2.			
DR ProDom; PD003649; Interleukin-2.			
DR SMART; SM00189; IL2; 1.			
DR PROSITE; PS00424; INTERLEUKIN-2; 1.			
SQ SEQUENCE 154 AA;	17652 MW;	4288D3D41D04F172 CRC64;	

Query Match 56.5%; Score 83; DB 2; Length 154;

Best Local Similarity 56.7%;	Pred. No. 0.00026;	Indels 0;	Gaps 0;
Matches 17; Conservative 6;	Mismatches 7;		

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OM protein - protein search, using sw model

Run on: September 23, 2005, 12:40:19 ; Search time 23.6066 Seconds

(without alignments)

122.275 Million cell updates/sec

Title: US-10-727-514-4

Perfect score: 147

Sequence: 1 APTSSSTKKTQLEHLLDQMLINGINN 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	100.0	153	1 ICG12	Interleukin-2 prec
2	147	100.0	153	1 ICH02	Interleukin-2 prec
3	114	77.6	154	2 JN0598	Interleukin 2 prec
4	97	66.0	155	2 A31278	Interleukin-2 prec
5	96	65.3	154	2 S16241	Interleukin-2 prec
6	95	64.6	155	2 S33509	Interleukin-2 - Mo
7	92	62.6	149	2 S31391	Interleukin-2 prec
8	79	53.7	155	2 I45913	Interleukin-2 prec
9	79	53.7	155	2 S38862	Interleukin-2 - go
10	79	53.7	155	2 S11488	Interleukin-2 prec
11	69	46.9	169	2 S37289	Interleukin-2 prec
12	64	43.5	169	1 ICM52	Interleukin-2 prec
13	59.5	40.5	60	2 I68870	Interleukin 2 - we
14	57.5	39.8	62	2 I54512	Interleukin 2 - mo
15	57.5	39.1	34.0	2 I68871	Interleukin 2 - mo
16	54	36.7	72	2 S12169	Isopenicillin N ac
17	52	35.4	737	2 G82262	probable exopolysa
18	51	34.7	304	2 P95285	probable LysR-type
19	51	34.7	627	2 E70122	flagellar hook-abs
20	50	34.0	365	2 C70701	hypothetical prote
21	49	33.3	543	2 F82217	methyl-accepting c
22	49	33.3	1130	2 A89130	protein F52a1.4 [i]
23	48.5	33.0	240	2 T22210	hypothetical prote
24	48	32.7	155	1 F64145	hypothetical prote
25	48	32.7	189	2 H64307	hypothetical prote
26	48	32.7	441	2 AB1367	probable transfera
27	48	32.7	441	2 AC1736	probable transfera
28	48	32.7	1061	1 GNLJG4	aminopeptidase C [
29	47.5	32.3	244	2 T11685	HIV-1 retropeptidase C [

30	47.5	32.3	938	2 F86548	polymorphic outer membrane
31	47	32.0	230	2 H27074	DNA-binding region
32	47	32.0	557	2 B70209	conserved hypothetical
33	47	32.0	1008	2 T41244	hypothetical prote
34	47	32.0	1964	2 AS9282	SEC14 protein homo
35	47	32.0	159	2 T05656	nonmuscle myosin I
36	47	31.6	211	2 C84888	hypothetical prote
37	46.5	31.6	293	2 A71946	hypothetical prote
38	46.5	31.6	323	2 H90434	hypothetical prote
39	46	31.3	380	1 C37760	galactokinase (EC
40	46	31.3	516	2 B64551	oligopeptide ABC transporter
41	46	31.3	571	2 H82355	hypothetical prote
42	46	31.3	614	2 T18745	hypothetical prote
43	46	31.3	692	2 T32980	hypothetical prote (cytosine-2-DNA)
44	46	31.3	1612	2 JC5210	hypothetical prote
45	46	31.3	3724	2 T18427	amino acid specific
46	46	31.0	466	2 B30228	hypothetical prote
47	46	30.6	307	2 T46103	pol polyprotein -
48	45	30.6	328	2 AC2415	conserved hypothetical
49	45	30.6	903	2 JB0327	dynamin-related protein
50	45	30.6	903	2 T50334	probable peptide A
51	45	30.6	333	2 S32114	probable acyltrans
52	45	30.6	1802	2 G71616	hypothetical prote
53	45	30.6	530	2 C89779	hypothetical prote
54	45	30.6	870	1 GNMYJA	hypothetical prote
55	45	30.6	2 F75608	2'-5A-dependent RNA	
56	45	30.6	44	2 T97167	3-isopropylmalate
57	45	30.6	903	2 G86015	phenylalanyl-tRNA
58	45	30.6	1802	2 B97167	hypothetical cell
59	44.5	30.3	359	2 T22950	flagellin family protein
60	44.5	30.3	511	2 S44275	two-component hybr
61	44.5	30.3	741	2 A45771	cinnamyl-alcohol d
62	44	29.9	269	2 G91169	3-isopropylmalate
63	44	29.9	273	2 G8607	phenylalanyl-tRNA
64	44	29.9	283	2 B97167	hypothetical prote
65	44	29.9	324	2 A97036	probable membrane
66	44	29.9	347	2 A12010	two-component hybr
67	44	29.9	357	2 S23526	cinnamyl-alcohol d
68	44	29.9	357	2 S23526	3-isopropylmalate
69	44	29.9	368	2 T46607	phenylalanyl-tRNA
70	44	29.9	474	2 B69494	hypothetical prote
71	44	29.9	487	2 A11146	F22D2.3 protein -
72	44	29.9	581	2 S09140	G Protein-coupled
73	44	29.9	585	2 T19814	probable integral
74	44	29.9	594	2 AB6309	probable integral
75	44	29.9	595	2 JC8012	hypothetical prote
76	44	29.9	627	2 S46820	probable integral
77	44	29.9	628	2 B91146	probable integral
78	44	29.9	628	2 F85991	hypothetical prote
79	44	29.9	715	2 G86634	probable integral
80	44	29.9	752	2 D40899	pol polyprotein -
81	44	29.9	943	2 S44636	F22D2.5 protein -
82	44	29.9	1019	2 T11560	pol polyprotein -
83	44	29.9	1034	2 D65119	acriflavin resistance
84	44	29.9	1050	2 AB0380	multidrug efflux P
85	44	29.9	1182	2 T30189	myelin transcriptri
86	44	29.9	1187	2 T46637	transcription fact
87	44	29.9	1188	2 E63310	zinc finger prote
88	44	29.9	1245	2 D71933	cinnamyl-alcohol d
89	43.5	29.6	1245	2 D71933	hypothetical prote
90	43.5	29.6	289	1 S75332	fibrillin - Synch
91	43.5	29.6	337	1 A37760	general stress pro
92	43	29.3	145	2 HB3921	probable transfera
93	43	29.3	152	2 T04479	probable glutathio
94	43	29.3	184	2 D71933	probable transfera
95	43	29.3	202	2 D71933	hypothetical prote
96	43	29.3	209	2 H69901	probable transfera
97	43	29.3	210	2 B85591	probable transfera
98	43	29.3	210	2 F64821	probable transfera
99	43	29.3	210	2 F90743	hypothetical prote
100	43	29.3	253	2 T15385	hypothetical prote

ALIGNMENTS

RESULT 1

ICG12

Interleukin-2 precursor - common gibbon
 N/Alternate names: IL-2; T-cell growth factor
 C/Species: Hylobates lar (common gibbon, white-handed gibbon)
 C/Accession: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 R/Chen, S.J.; Holbrook, N.J.; Mitchell, K.F.; Vallone, C.A.; Crabtree, P.; Natl. Acad. Sci. U.S.A. 82, 7284-7288, 1985
 A/Title: A viral long terminal repeat in the interleukin 2 gene of a cell line that contains a reference number: A94067; MUID:3877307
 A/Accession: A94067
 A/Molecule type: mRNA
 A/Residues: 1-153 <C>H>
 A/Cross-references: UNIPROT:P60569; GB:M11144; NID:9177014; PIDN:AAA35454.1; PID:9177015
 A/Experimental source: leukemia cell line MLA 144; ATCC TIB 201
 A/Note: the integration of a retrovirus sequence containing a 5'LTR into the 3' noncoding region of interleukin-2
 C/Supfamily: interleukin-2
 C/Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell
 F/1-20/Domain: signal sequence #status predicted <SG>
 F/21-153/Product: interleukin-2 #status predicted <IL2>
 F/23/Binding site: carbohydrate (thr) (covalent) #status Predicted
 F/78-125/Diulfide bonds: #status predicted

A;Residues: 11-117 <LAA>
 A;Cross-references: EMBL:Z14955

A;Note: this sequence is shown from the beginning of the fragment to the chromosomal break R; Taniguchi, T.; Matsui, H.; Fujita, T.; Takaoka, C.; Kashima, N.; Yoshimoto, R.; Hamuro Nature 302, 305-310, 1983
 A/Title: Structure and expression of a cloned cDNA for human interleukin-2.
 A/Reference number: A93297; MUID:33167172; PMID:6403867
 A/Accession: A93297
 A/Molecule type: mRNA
 A/Residues: 1-153 <TAN>
 A/Cross-references: GB:V00564; NID:933780; PIDN:CAA23827.1; PID:933781
 A/Experimental source: leukemic T-cell line Jurkat-111, cloned from Jurkat-FHRCR R; Maeda, S.; Nishino, N.; Obaru, K.; Mita, S.; Nomiyama, H.; Shimada, K.; Fujimoto, K.; Biochem. Biophys. Res. Commun. 115, 1040-1047, 1983
 A/Title: Cloning of interleukin 2 mRNAs from human tonsils
 A/Reference number: A90113; MUID:84023840; PMID:6312994
 A/Accession: A90113
 A/Molecule type: mRNA
 A/Residues: 1-153 <NAB>
 A/Cross-references: GB:J00264; NID:9186294; PIDN:AAD48509.1; PID:95729676
 A/Experimental source: costimulatory monocellular cells R; Eisenberg, O.; Faber-Elman, A.; Remau, R; Devos, R.; Plaetinck, G.; Cheroutre, H.; Simons, G.; Degrave, W.; Tavernier, J.; Remaury, J. Neurochem. 64, 1928-1936, 1995
 Nucleic Acids Res 11, 4307-4323, 1983
 A/Title: Molecular cloning of human interleukin 2 cDNA and its expression in Escherichia
 A/Reference number: A93478; MUID:83246551; PMID:6306584
 A/Accession: A93478
 A/Molecule type: mRNA
 A/Residues: 1-153 <DBV>
 A/Cross-references: GB:V00564; NID:933780; PIDN:CAA23827.1; PID:933781
 A/Experimental source: epilenoocytes R; Eisenberg, O.; Lotan, M.; Schwartz, M.
 A/Title: Interleukin-2 transcripts in human and rodent brains: possible expression by as A/Reference number: 156518; MUID:5239150; PMID:7722480
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-152 <BIZ>
 A/Cross-references: GB:S77834; NID:9999000
 A/Accession: 173624
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 5-7, P, 9-17, 'P', 19-32, 'X', 34-45, 'X', 47-143 <REBS>
 A/Cross-references: GB:S77835; NID:999001; PIDN:AAD142264.1; PMID:94221964
 R;Nishino, N.; Obaru, K.; Meda, S.; Shimada, K.; Onoue, K.
 Biomed. Res. 6, 197-205, 1985
 A/Title: Organization of the DNA regions flanking the human interleukin 2 gene.
 A/Reference number: 157003; MUID:8706418; PMID:1491296
 A/Accession: 152528
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-68 <REB2>
 A/Cross-references: GB:M33199; NID:9186296; PIDN:AAA59139.1; PID:9553508
 R;Siebenlist, U.; Durand, D.B.; Bressler, P.; Holbrook, N.J.; Norris, C.A.; Kamoun, M.; Mol. Cell. Biol. 6, 3042-3047, 1986
 A/Title: Promoter region of interleukin-2 gene undergoes chromatin structure changes and A/Reference number: 157003; MUID:8706418; PMID:1491296
 A/Accession: 157603
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-68 <REB3>
 A/Cross-references: GB:M13879; NID:9186305; PIDN:AAA59141.1; PID:9553509
 R;Weir, M.P.; Chaplin, M.A.; Wallace, C.W.; Hobden, A.N.; Biochemistry 27, 688-689, 1988
 A/Title: Structure-activity relationships of recombinant human interleukin 2.
 A/Reference number: 152401; MUID:89062420; PMID:13264184
 A/Accession: 152401
 A/Molecule type: DNA
 A/Residues: 1-153 <FJU>
 A/Cross-references: GB:J00264; NID:9186294; PIDN:AAA59141.1; PID:9553509
 R;Holbrook, N.J.; Smith, K.A.; Fornace Jr., A.J.; Comeau, C.M.; Wiskocil, R.L.; Crabtree, Proc. Natl. Acad. Sci. U.S.A. 80, 7437-7441, 1983
 A/Title: Structure of the human interleukin-2 gene.
 A/Reference number: A20961; MUID:84170356; PMID:6608729
 A/Molecule type: DNA
 A/Accession: A20961
 A/Molecule type: DNA
 A/Residues: 1-153 <HO2>
 A/Cross-references: GB:K02056; NID:9186302; PIDN:AAA98792.1; PID:9386819
 R;Laabi, Y.; Gras, M.P.; Carboneil, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tapias, EMBO J. 11, 3897-3904, 1992
 A/Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t (4;1
 A/Reference number: S312008; MUID:93010984; PMID:1396583
 A/Accession: S312008
 A/Molecule type: mRNA

RESULT 2

ICG12

Interleukin-2 precursor [validated] - human

N/Alternate names: IL-2; T-cell growth factor

C/Species: Homo sapiens (man)

C/Accession: 11-Aug-1983 #sequence_revision 11-Aug-1983 #text_change 09-Jul-2004

R;Holbrook, N.J.; Lieber, M.; Crabtree, G.R.

Nucleic Acids Res. 12, 5005-5013, 1984

A/Title: DNA sequence of the 5'-flanking region of the human interleukin 2 gene: homolog

A/Accession: A01849

A/Molecule type: DNA

A/Residues: 1-153 <HOU>

A/Cross-references: UNIPROT:P60568; GB:X00695; GB:X00200; GB:X00201; NID:9337

R;Fujita, T.; Takaoka, C.; Matsui, H.; Taniguchi, T.

Proc. Natl. Acad. Sci. U.S.A. 80, 7437-7441, 1983

A/Title: T-cell growth factor: complete nucleotide sequence and organization of the gene

A/Reference number: A20961; MUID:84170356; PMID:6608729

A/Molecule type: DNA

A/Residues: 1-153 <FJU>

A/Cross-references: GB:J00264; NID:9186294; PIDN:AAA59141.1; PID:9553509

R;Laabi, Y.; Gras, M.P.; Carboneil, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tapias, EMBO J. 11, 3897-3904, 1992

A/Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t (4;1

A/Reference number: S312008; MUID:93010984; PMID:1396583

A/Accession: S312008

A/Molecule type: mRNA

R;Robb, R.J.; Kurtny, R.M.; Panico, M.; Morris, H.R.; Chowdhry, V.
 Proc. Natl. Acad. Sci. U.S.A. 81, 6486-6490, 1984
 A;Title: Amino acid sequence and post-translational modification of human interleukin 2.
 A;Reference number: A94009; MUID:85038540; PMID:6333684

A;Molecule type: protein

A;Residues: 21-153 <RQB>

A;Note: disulfide bonds and carbohydrate binding site were determined in lacking 21-Ala (FT-IL2-A and FT-IL2-B) and 22-Pro (FT-IL2-B)
 R;Conradt, H.S.; Nimitz, M.; Dittmar, K.E.J.; Lindemann, W.; Hoppe, J.; Hauser, H.
 J. Biol. Chem. 264, 17368-17373, 1989
 A;Title: Expression of human interleukin-2 in recombinant baby hamster kidney, Ltk-, and de.
 A;Reference number: A34463; MUID:90008901; PMID:2793860

A;Accession: A34463

A;Molecule type: protein

A;Residues: 21-35 <CON>

A;Note: the O-linked glycosylation site in recombinant material matched that from human R;Grabenhorst, B.; Hoerl, B.; Nimitz, M.; Jaeger, V.; Conradt, H.S.
 Eur. J. Biochem. 215, 189-197, 1993
 A;Title: Biosynthesis and secretion of human interleukin 2 glycoproteins variants from b
 A;Reference number: S34025; MUID:9334549; PMID:8344280
 A;Contents: annotation; glycosylation of variant forms expressed in insect cells
 C;Genetics:
 A;Gene: GDB: IL2
 A;Cross-references: GDB:119344; OMIN:147680

A;Map position: 4q26.4q27

A;Introns: 49/3; 69/3; 117/3

C;Superfamily: interleukin-2

C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell
 P;1-20/Domain: signal sequence #status predicted <SIG>
 P;21-153/Product: interleukin-2 #status experimental <IL2>
 P;23/Binding site: carbohydrate (thr) (covalent) #status experimental
 P;78-125/Disulfide bonds: #status experimental

Query Match Score 100.0%; Best Local Similarity 100.0%; Pred. No. 2.3e-14; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 APTSSSTKTKTQLEHLLDQMLINGINN 30
 Db 21 APTSSSTKTKTQLEHLLDQMLINGINN 50

RESULT 3

JN0698

Interleukin 2 precursor - cat

C;Species: Felis silvestris catus (domestic cat)

C;Accession: JN0698

R;Cozzi, P.J.; Padrid, P.A.; Takeda, J.; Allegre, M.L.; Yuhki, N.; Leff, A.R.
 Biochem. Biophys. Res. Commun. 194, 1038-1043, 1993
 A;Title: Sequence and functional characterization of feline interleukin 2.
 A;Reference number: JN0698; MUID:93356765; PMID:8352761
 A;Accession: JN0698
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:Li19402; NID:9304313; PID:9304314
 C;Superfamily: interleukin-2
 C;Keywords: growth factor

Query Match Score 114; Best Local Similarity 73.3%; Pred. No. 1.8e-09; Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 APTSSSTKTKTQLEHLLDQMLINGINN 30
 Db 21 APASSSTKETQQOLEQQLLDRLLLNVNN 50

RESULT 4

S33509

Interleukin-2 - Mongolian jird

C;Species: Meriones unguiculatus (Mongolian jird)

C;Accession: S33509

R;Mai, Z.; Klei, T.; Horchov, D.

submitted to the EMBL Data Library, October 1992

A;Description: Cross-species PCR cloning of Jird (Meriones unguiculatus) interleukin-2 c

A31278
 interleukin-2 precursor - rat
 N;Alternate names: IL-2; T-cell growth factor
 C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Apr-1989 #sequence_revision 26-Apr-1989

C;Accession: A55882; A31278

R;McKnight, A.J.; Maesn, D.W.; Barclay, A.N.

Immunogenetics 30, 145-147, 1989

A;Title: Sequence of rat interleukin 2 and anomalous binding of a mouse interleukin 2 c

A;Reference number: A45882; MUID:89339608; PMID:2788130

A;Accession: A55882

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-155 <NCNK>

A;Cross-references: UNIPROT:PI1708; GB:M22899; NID:9204909; PID:9204910

C;Superfamily: interleukin-2

C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell

C;Accession: A55882

Query Match Score 97; DB 2; Length 155;

Best Local Similarity 66.7%; Pred. No. 6e-07;

Matches 20; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 APTSSSTKTKTQLEHLLDQMLINGINN 30

Db 21 APTSSPAKETQQLLEQQLLQLLQVLLRGIDN 50

RESULT 5

S16241

Interleukin-2 precursor - pig

N;Alternate names: IL-2; T-cell growth factor

C;Species: Sus scrofa domestica (domestic pig)

C;Accession: S16241; S15473

R;Goodall, J.C.; Emery, D.C.; Bailey, M.; English, L.S.; Hall, L.

Biochim. Biophys. Acta 1089, 257-258, 1991

A;Title: cDNA cloning of porcine interleukin 2 by polymerase chain reaction.

A;Reference number: S16241; MUID:91274360; PMID:2054386

A;Accession: S16241

A;Molecule type: mRNA

A;Residues: 1-154 <GOO>

A;Cross-references: UNIPROT:P26891; EMBL:X58650; NID:91991; PID:CAA40071.1; PMID:91992

R;LeFevre, F.

Submitted to the EMBL Data Library, March 1991

A;Description: Molecular cloning of porcine interleukin 2 cDNA by the polymerase chain r

A;Reference number: S15473

A;Accession: S15473

A;Molecule type: mRNA

A;Residues: 1-154 <LEFB>

C;Superfamily: interleukin-2

C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell

F;21-20/Domain: signal sequence #status predicted <SIG>

F;21-154/Product: interleukin-2 #status predicted <MAT>

Query Match Score 96; DB 2; Length 154;

Best Local Similarity 66.7%; Pred. No. 8.4e-07;

Matches 20; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 APTSSSTKTKTQLEHLLDQMLINGINN 30

Db 21 APTSSPAKETQQLLEQQLLQLLQVLLRGIDN 50

RESULT 6

S33509

Interleukin-2 - Mongolian jird

C;Species: Meriones unguiculatus (Mongolian jird)

C;Accession: S33509

R;Mai, Z.; Klei, T.; Horchov, D.

submitted to the EMBL Data Library, October 1992

A;Description: Cross-species PCR cloning of Jird (Meriones unguiculatus) interleukin-2 c

A;Reference number: S33509
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-155 <AN>
 A;Cross-references: UNIPROT:Q08081; EMBL:X68779; NID:g577588; PIDN:CAA48679.1; PID:93116
 C;Superfamily: interleukin-2

RESULT 9
 S38662
 Query Match 64.6%; Score 95; DB 2; Length 155;
 Best Local Similarity 66.7%; Pred. No. 1.2e-06;
 Matches 20; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 Qy 1 APTSSSTKTKTQOLEHILLDQMLINGINN 30
 Db 21 APTSSPAKEAQYEQILLDQMLQVRINN 50

RESULT 7
 S31391
 interleukin-2 precursor - horse
 C;Species: Equus caballus (domestic horse)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S31391
 R;Tavernor, A.S.; Butcher, G.W.
 submitted to the EMBL Data Library, November 1992
 A;Description: cDNA cloning of equine interleukin-2 by polymerase chain reaction.
 A;Reference number: S31391
 A;Accession: S31391
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-149 <TAV>
 A;Cross-references: UNIPROT:P37997; EMBL:X69393; NID:g1076; PIDN:CAA49190.1; PID:g1077
 C;Superfamily: interleukin-2

Query Match 64.6%; Score 92; DB 2; Length 149;
 Best Local Similarity 65.7%; Pred. No. 3.2e-06;
 Matches 17; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 APTSSSTKTKTQOLEHILLDQMLINGINN 30
 Db 21 APTSSSKRETQOOLKQMDLKLLREGVNN 50

RESULT 8
 I45913
 interleukin-2 precursor - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
 C;Accession: I45913; S21470; S20761
 R;Cerrett, D.P.; McKerigan, K.; Larsen, A.; Cantrell, M.A.; Anderson, D.; Gillis, S.;
 Proc. Natl. Acad. Sci. U.S.A. 83: 3223-3227, 1986
 A;Title: Cloning, sequence, and expression of bovine interleukin 2.
 A;Accession number: 145913; MUD:8605869; PMID:3517854
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-155 <CPR>
 A;Cross-references: UNIPROT:P05016; GB:M12791; NID:g163204; PIDN:AAA30586.1; PID:g163205
 R;Anikeeva, N.N.; Vinogradova, T.V.; Votoshin, O.N.
 Submitted to the EMBL Data Library, December 1989
 A;Reference number: S21470
 A;Accession: S21470
 A;Molecule type: DNA
 A;Residues: 1-22 <AN>
 A;Cross-references: EMBL:X17201; NID:g9452; PIDN:CAA35062.1; PID:g9453
 C;Genetics:
 C;Superfamily: interleukin-2

Query Match 53.7%; Score 79; DB 2; Length 155;
 Best Local Similarity 53.3%; Pred. No. 0.00028;
 Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 APTSSSTKTKTQOLEHILLDQMLINGINN 30
 Db 21 APTSSSTGNTMKEVSSLDDQMLKEVNN 50

Qy 1 APTSSSTKTKTQOLEHILLDQMLINGINN 30
 Db 21 APTSSSTGNTMKEVSSLDDQMLKEVNN 50

RESULT 9
 S38662
 interleukin-2 - goat
 C;Species: Capra aegagrus hircus (domestic goat)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 R;Rimstad, E.
 submitted to the EMBL Data Library, November 1993
 A;Description: The molecular cloning and expression of caprine interleukin 2.
 A;Reference number: S38662
 A;Accession: S38662
 A;Molecule type: mRNA
 A;Residues: 1-155 <PIM>
 A;Cross-references: UNIPROT:P36835; EMBL:X76063; NID:g416002; PIDN:CAA53664.1; PID:g41600
 C;Superfamily: interleukin-2

Query Match 53.7%; Score 79; DB 2; Length 155;
 Best Local Similarity 53.3%; Pred. No. 0.00028;
 Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 APTSSSTKTKTQOLEHILLDQMLINGINN 30
 Db 21 APTSSSTGNTMKEVSSLDDQMLKEVNN 50

RESULT 10
 S11488
 interleukin-2 precursor - sheep
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S11488; S13102; S15517
 R;Seow, H.F.; Rothel, J.S.; Padford, A.J.; Wood, P.R.
 Nucleic Acids Res. 18, 7175, 1990
 R;Goodall, J.C.; Emery, D.C.; Perry, A.C.F.; English, L.S.; Hall, L.
 Nucleic Acids Res. 18, 5883, 1990
 A;Title: cDNA cloning of ovine interleukin 2 by the polymerase chain react
 A;Reference number: S13102; MUD:9108836; PMID:2263496
 A;Accession: S11488
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-155 <S00>
 A;Cross-references: UNIPROT:P19114; EMBL:X53934; NID:g1281; PIDN:CAA37881.1; PID:g1282
 R;Seow, H.F.; Rothel, J.S.; Padford, A.J.; Wood, P.R.
 Nucleic Acids Res. 18, 7175, 1990
 A;Title: The molecular cloning of ovine interleukin 2 gene by the polymerase chain react
 A;Reference number: S13102; MUD:9108836; PMID:2263496
 A;Accession: S11488
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-5,'L',7-155 <S00>
 A;Cross-references: EMBL:X56100; NID:g1810; PIDN:CAA39165.1; PID:g1811
 R;Buidoso, R.; Williamson, M.L.; Sargent, D.R.; Hein, W.H.; McConnell, L.
 Submitted to the EMBL Data Library, April 1991
 A;Accession: S15517
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 21-153 <BUU>
 A;Cross-references: EMBL:X60448
 C;Superfamily: interleukin-2

Query Match 53.7%; Score 79; DB 2; Length 155;
 Best Local Similarity 53.3%; Pred. No. 0.00028;
 Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

A;Molecule type: DNA
 A;Residues: 1-62 <RES>
 A;Cross-references: GB:L07574; NID:9349513; PIDN:AAA39326.1; PID:9349514
 C;Genetics:
 A;Gene: IL-2
 C;Superfamily: interleukin-2

Query Match 39.8%; Score 58.5; DB 2; Length 62;
 Best Local Similarity 42.9%; Pred. No. 0.11; 9; Gaps 1;
 Matches 15; Conservative 6; Mismatches 5; Indels 9; Gaps 1;

Qy 1 APTSSST-----KTKTQLOLEHLLIDLQMLN 26
 Db 25 SPTSSSTSSATAQQQQQHQLEQIIMDQFLS 59

RESULT 15
 I68871
 Interleukin 2 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: I68871
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
 R;Matesanz, F.; Alcina, A.; Pellicer, A.
 Immunogenetics 38, 300-303, 1993
 A;Title: Existence of at least five interleukin-2 molecules in different mouse strains.
 A;Reference number: 154512; MUID:9330793; PMID:8319981
 A;Accession: I68871
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-72 <RES>
 A;Cross-references: GB:L07576; NID:9349517; PIDN:AAA39328.1; PID:9349518
 C;Genetics:
 A;Gene: IL-2
 C;Superfamily: interleukin-2

Query Match 39.1%; Score 57.5; DB 2; Length 72;
 Best Local Similarity 35.6%; Pred. No. 0.18; 5; Gaps 1;
 Matches 16; Conservative 5; Mismatches 5; Indels 19; Gaps 1;

Qy 1 APTSSSTKTKTQLQ-----LEHLLIDLQMLN 26
 Db 25 SPTSSSTSSATAQQQQQHQLEQIIMDQFLS 69

RESULT 16
 S12169
 Isopenicillin N acyltransferase (EC 2.3.1.--) - *Emericella midulans*
 N;Alternate names: acyl coenzyme A-6-aminopenicillanic acid acyltransferase; acyltransferase
 C;Species: *Emericella midulans*, *Aspergillus nidulans*
 C;Accession: S12169; A36142; S09090
 C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 R;Montenegro, E.; Barredo, J.L.; Gutierrez, S.; Diez, B.; Alvarez, E.; Martin, J.F.
 Mol. Gen. Genet. 221, 322-330, 1990
 A;Title: Cloning, characterization of the acyl-CoA:6-amino penicillanic acid acyltransferase
 A;Reference number: S12169; MUID:90340281; PMID:2166227
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-357 <MON>
 A;Cross-references: UNIPROT: P21133; EMBL:X53310; NID:92378; PIDN:CAA37394.1; PID:92379
 R;Tobin, M.B.; Fleming, M.D.; Skatrud, P.L.; Miller, J.R.
 J. Bacteriol. 172, 5908-5914, 1990
 A;Title: Molecular characterization of the acyl-coenzyme A:isopenicillin N acyltransferase
Escherichia coli.
 A;Reference number: A36142; MUID:91008967; PMID:2120195
 A;Accession: A36142
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-357 <TOB>
 A;Cross-references: GB:M512293; NID:9167999; PIDN:AAA33387.1; PID:9168000
 R;Whiteman, P.A.; Abrahams, E.P.; Baldwin, J.E.; Fleming, M.D.; Schofield, C.J.; Sutherland, P.; Vandenhout, M.; Vorholter, P.J.; Weiland, D.H.; Wong, K.; Yeh, K.
 FEBS Lett. 262, 342-344, 1990
 A;Title: The composite genome of the *legume symbiont Sinorhizobium meliloti*.
 A;Reference number: A96039; MUID:2136834; PMID:11474104

A;Reference number: S09089; MUID:90242961; PMID:2110531
 A;Accession: S09090
 A;Molecule type: protein
 A;Residues: 103-122 <WHI>
 C;Genetics:
 A;Introns: 12/3; 71/1; 121/3
 C;Keywords: acyltransferase

Query Match 36.7%; Score 54; DB 2; Length 357;
 Best Local Similarity 52.6%; Pred. No. 3.6; 5; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TKTKTQLOLEHLLIDLQMLN 25
 Db 40 TKTKTQLEQIIREEQVM 58

RESULT 17
 G82262
 probable exopolysaccharide biosynthesis protein VC0937 [imported] - *Vibrio cholerae* (strain 139)

C;Species: *Vibrio cholerae*
 C;Accession: G82262
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 R;Heidelberger, J.P.; Eisen, J.A.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Brmojaeva, M.D.; Vanathavan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; Fraser, C.M.
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Reference number: A82035; MUID:20406333; PMID:10952301
 A;Accession: G82262
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-37 <HEI>
 A;Cross-references: UNIPROT:Q9KTG5; GB:AE004176; GB:AE003882; NID:99655385; PIDN:AAF9409
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VC0937
 A;Map position: 1

Query Match 35.4%; Score 52; DB 2; Length 737;
 Best Local Similarity 39.4%; Pred. No. 16; 4; Mismatches 12; Indels 4; Gaps 1;

Qy 2 PTSSSTKTKTQLQ-----HLLDQMLN 30
 Db 330 PKHPKIKSASQLEAVRKNLRAELQQLNGINN 362

RESULT 18
 F95285
 probable LySR-type regulator [imported] - *Sinorhizobium meliloti* (strain 1021) magaPlasm

C;Species: *Sinorhizobium meliloti*
 C;Accession: F95285
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barlow, P.; Bows; Peck, M.; Surzycki, R.; Weilis, D.H.; Yeh, K.C.
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A;Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti* magaPlasm
 A;Reference number: A95262; MUID:2139659; PMID:11481432
 A;Accession: F95285
 A;Molecule type: DNA
 A;Residues: 1-304 <KUR>
 A;Cross-references: UNIPROT:Q930K5; GB:AE006469; PIDN:AAK61848.1; PID:914523262; GSPBB:G
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barlow-Hubler, P.; Celia, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komo, C.; Lelaure, Rebault, P.; Vandenhout, M.; Vorholter, P.J.; Weiland, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the *legume symbiont Sinorhizobium meliloti*.
 A;Reference number: A96039; MUID:2136834; PMID:11474104

A:Contents: annotation
 C:Genetics:
 A:Gene: SMA0353
 A:Genome: plasmid

Query Match 34.7%; Score 51; DB 2; Length 304;
 Best Local Similarity 48.1%; Pred. No. 8.4;
 Matches 13; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

Qy 6 STRKKQLEQ-HULLDQMLNGINN 30
 Db 58 STRKKQLEQTLGRYTLAARSVNGIDN 84

RESULT 19
 E70122 flagellar hook-associated protein (flgK) homolog - Lyme disease spirochete
 C:Species: *Borrelia burgdorferi* (Lyme disease spirochete)
 C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
 C:Accession: E70122
 R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, S.; Bowman, C.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, J.; Nature 390, 580-586, 1997
 A:Authors: Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Hatch, B.; Venter, J.C.
 A:Title: Genomic sequence of Lyme disease spirochete, *Borrelia burgdorferi*.
 A:Reference number: A70100; MUID:98065943; PMID:9403685
 A:Accession: E70122
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-627 <KLE>
 A:Cross-references: UNIPROT:P70859; GB:AE0001129; PIDN:92688071; NID:92688073; PIDN: AAC6657
 A:Experimental source: strain B31

Query Match 34.7%; Score 51; DB 2; Length 627;
 Best Local Similarity 42.3%; Pred. No. 19;
 Matches 11; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 4 SSSTTKTQLEHULLDQMLNGIN 29
 Db 564 SEITKESSQILKDLTDLMSISGVN 589

RESULT 20
 C70701 hypothetical protein Rv0029 - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: C70701
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Ralbandre, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Shelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A:Authors: Squires, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A05000; MUID:9825987; PMID:9634230
 A:Accession: C70701
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-365 <COL>
 A:Cross-references: UNIPROT:P71599; GB:Z80233; PIDN:93261645; PIDN: CAB02414.
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: Rv029

Query Match 34.0%; Score 50; DB 2; Length 365;
 Best Local Similarity 40.0%; Pred. No. 15;
 Matches 12; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 1 APPSSSTKTKTQLEHULLDQMLNGIN 30
 Db 43 AELSSNTATATLAEHLRIVGSAND 72

RESULT 21
 FR2217 methyl-accepting chemotaxis protein VC1238 [imported] - *Vibrio cholerae* (strain N16961 :
 C:Species: *Vibrio cholerae*
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: FR2217
 R:Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardom, D.; Brumfitt, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, J., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A:Reference number: A82035; MUID:20406833; PMID:20406833; PMID:10952301
 A:Accession: FR2217
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-543 <HEI>
 A:Cross-references: UNIPROT:Q9KSF8; GB:AE003852; NID:99655779; PIDN:AAF944
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 A:Genetics:
 A:Gene: VC1238
 A:Map position: 1

Query Match 33.3%; Score 49; DB 2; Length 543;
 Best Local Similarity 37.5%; Pred. No. 32;
 Matches 9; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 3 TSSSTKTKTQLEHULLDQMLIN 26
 Db 506 SASETRISIDLEHLSQLESIN 529

RESULT 22
 A89130 protein F52B1.4 [imported] - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
 C:Accession: A89130
 R:anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
 A:Reference number: A75000; MUID:99069613; PMID:9051916
 A:Note: See websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
 A:Accession: A89130
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1130 <STO>
 A:Cross-references: GB:chr_V; PIDN: AAB37038.1; PID:91086805; GSPDB:GN00023; CESP:F52B1.4
 C:Genetics:
 A:Gene: F52B1.4
 A:Map position: 5
 C:Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain home
 Query Match 33.3%; Score 49; DB 2; Length 1130;
 Best Local Similarity 46.2%; Pred. No. 72;
 Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 3 TSSSTKTKTQLEHULLDQMLIN 28
 Db 906 TLLASRCTPLQVNLNDLVTTIFDGI 931

RESULT 23
 T22210 hypothetical protein F44G1.7 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T22210
 R:Sims, M.
 A:Submitted to the EMBL Data Library, June 1995
 A:Reference number: Z19530
 A:Accession: T22210

A;Status: preliminary; translated from GB/EMBL/DBJ	Best Local Similarity 32.1%; Pred. No. 14; Matches 9; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
A;Molecule type: DNA	
A;Residues: 1-240 <WIL>	
A;Cross-references: UNIPROT:Q20417; EMBL:249910; PIDN:CAA90123.1; GSPDB:GN00020; CESP:FA	
A;Experimental source: Clone F44G4.7	
C;Genetics:	
A;Gene: CESP:F44G4.7	
A;Map position: 2	
A;Introns: 123/2; 159/3	
C;Superfamily: <i>Caenorhabditis elegans</i> hypothetical protein F44G4.7	
Query Match 33.0%; Score 48.5; DB 2; Length 240; Best Local Similarity 44.0%; Pred. No. 15; Matches 11; Conservative 9; Mismatches 4; Indels 1; Gaps 1;	
Qy 2 PESSSTKTKTQLEHLLLDLQMLIN 26	
Db 146 PTSSQEQREKWRVK-LJJDLEMILS 169	
RESULT 24	
hypothetical protein H0227 - <i>Haemophilus influenzae</i> (strain Rd KW20)	
C;Species: <i>Haemophilus influenzae</i>	
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004	
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Cocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.J.; Geohagen, N.S.M.; Science 269, 496-512, 1995	
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Reference number: A640000; PMID:95350630; PMID:7542800	
A;Accession: F64145	
A;Molecule type: DNA	
A;Residues: 1-155 <TRIG>	
A;Cross-references: UNIPROT:P44583; GB:U32709; NID:gi1573190; PIDN: AAC21897.1;	
C;Superfamily: hypothetical protein H0227	
Query Match 32.7%; Score 48; DB 1; Length 155; Best Local Similarity 27.6%; Pred. No. 11; Matches 8; Conservative 8; Mismatches 13; Indels 0; Gaps 0;	
Qy 2 PSSSTKTKTQLEHLLLDLQMLINGIN 30	
Db 52 PETAEPSSKKAAELHHEYDQVQLRGTE 80	
RESULT 25	
hypothetical protein MJ0064 - <i>Methanococcus jannaschii</i>	
C;Species: <i>Methanococcus jannaschii</i>	
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004	
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, i; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Rison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Hurst, M.A.	
Science 275, 1058-1073, 1996	
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.	
A;Title: Complete genome sequence of the methanogenic archaeon, <i>Methanococcus jannaschii</i>	
A;Reference number: A643000; MUID:96337998; PMID:8688087	
A;Accession: H64307	
A;Molecule type: nucleic acid	
A;Residues: 1-189 <BUT>	
A;Cross-references: UNIPROT:Q60376; GB:U67464; PIDN: AAB98051.1;	
C;Genetics:	
A;Map position: FOR61888-62457	
A;Start codon: GTG	
Query Match 32.7%; Score 48; DB 2; Length 189;	

A;Status: preliminary; translated from GB/EMBL/DBJ	Best Local Similarity 32.1%; Pred. No. 14; Matches 9; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
A;Molecule type: DNA	
A;Residues: 1-240 <WIL>	
A;Cross-references: UNIPROT:Q20417; EMBL:249910; PIDN:CAA90123.1; GSPDB:GN00020; CESP:FA	
A;Experimental source: Clone F44G4.7	
C;Genetics:	
A;Gene: CESP:F44G4.7	
A;Map position: 2	
A;Introns: 123/2; 159/3	
C;Superfamily: <i>Caenorhabditis elegans</i> hypothetical protein F44G4.7	
Query Match 33.0%; Score 48.5; DB 2; Length 240; Best Local Similarity 44.0%; Pred. No. 15; Matches 11; Conservative 9; Mismatches 4; Indels 1; Gaps 1;	
Qy 2 PESSSTKTKTQLEHLLLDLQMLIN 26	
Db 146 PTSSQEQREKWRVK-LJJDLEMILS 169	
RESULT 26	
aminopeptidase C [imported] - <i>Listeria monocytogenes</i> (strain EGDe-e)	
C;Species: <i>Listeria monocytogenes</i>	
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004	
C;Accession: AB13367	
R;Glaser, P.; Prangueul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker ;; Dominguez-Bernal, G.; Duchaude, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.	
Science 294, 849-852, 2001	
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madiueno, E.; Vazquez-Boland, J.A.; Maitouram, A.; Wehland, C.; Schluefer, T.; Simoes, N.; Tierrez, A.; Voss, H.; Wehland, A;Title: Comparative Genomics of <i>Listeria</i> species	
A;Reference number: AB1077; MUID:21537279; PMID:11679669	
A;Status: preprint	
A;Molecule type: DNA	
A;Accession: AB13367	
A;Residues: 1-441 <GLA>	
A;Cross-references: UNIPROT:069192; GB:NC_003210; PIDN: CAD00416.1; PID:gi16411826; GSPDB:..	
A;Experimental source: strain EGDe-e	
A;Genetics:	
C;Superfamily: aminopeptidase C (bleomycin hydrolase)	
Query Match 32.7%; Score 48; DB 2; Length 441; Best Local Similarity 34.6%; Pred. No. 36; Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;	
Qy 4 SSSTKTKTQLEHLLLDLQMLINGIN 29	
Db 344 TATTAERDQYKSHMLTHAMVLTGYN 369	
RESULT 27	
aminopeptidase C [imported] - <i>Listeria innocua</i> (strain Clip11262)	
C;Species: <i>Listeria innocua</i>	
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004	
C;Accession: AC1736	
R;Glaser, P.; Prangueul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker ;; Dominguez-Bernal, G.; Duchaude, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.	
Science 294, 849-852, 2001	
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madiueno, E.; Vazquez-Boland, J.A.; Maitouram, A.; Wehland, C.; Schluefer, T.; Simoes, N.; Tierrez, A.; Voss, H.; Wehland, A;Title: Comparative Genomics of <i>Listeria</i> species	
A;Reference number: AB1077; MUID:21537279; PMID:11679669	
A;Status: preprint	
A;Molecule type: DNA	
A;Accession: AC1736	
A;Residues: 1-441 <GLA>	
A;Cross-references: UNIPROT:0928V0; GB:AL592022; PIDN: CAC97659.1; PID:gi16414954; GSPDB:G	
A;Experimental source: strain Clip11262	
A;Genetics:	
C;Superfamily: aminopeptidase C (bleomycin hydrolase)	
Query Match 32.7%; Score 48; DB 2; Length 441; Best Local Similarity 34.6%; Pred. No. 36; Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;	
Qy 4 SSSTKTKTQLEHLLLDLQMLINGIN 29	
Db 344 TATTAERDQYKSHMLTHAMVLTGYN 369	

RESULT 28
 Q9NQJ4
 HIV-1 retropepsin (BC 3.4.23.16) - simian immunodeficiency virus (African green monkey) i
 N: Contains: endonuclease (EC 3.1.1.1); retropepsin (EC 3.4.23.16); RNA-directed DNA pol
 C: Species: simian immunodeficiency virus, SIV
 C: Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 03-Jun-2002
 C: Accession: B30045
 R: Fukasawa, M.; Miura, T.; Hasegawa, A.; Morikawa, S.; Tsujimoto, H.; Miki, K.; Kitamura
 Nature 333, 457-461, 1988
 A: Title: Sequence of simian immunodeficiency virus from African green monkey, a new memb
 A: Reference number: A30045; MUID:88232906; PMID:3374586
 A: Accession: B30045
 A: Molecule type: DNA
 A: Residues: 1-1061 <RTR>
 A: Cross-references: EMBL:207805; NID:961148; PID:gi1335593
 C: Comments: Specific enzymatic cleavages may yield mature proteins including protease, re
 C: Genetics:
 A: Gene: pol
 C: Superfamily: polypolyprotein
 C: Keywords: aspartic proteinase; hydrolase; nucleotidyltransferase; polypeptide; reverse
 P,111-210/Product: retropepsin #status predicted <RTP>
 P,134/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 32.7% Score 48; DB 1; Length 1061;
 Best Local Similarity 52.9%; Pred. No. 95%;
 Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Q9 10 TQQLQHLLLDQMLIN 26
 Db 976 TQLBIQHQLTKIQKILN 992

RESULT 29
 T11685
 hypothetical protein SPBC21D10.13 SPBC1921.07c - fission yeast (Schizosaccharomyces pombe)
 C: Species: Schizosaccharomyces pombe
 C: Date: 16-Jul-1999 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 R: Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 A: Reference number: T11685
 A: Accession: T11685
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 A: Residues: 1-155 <SER>
 A: Cross-references: UNIPROT:Q9U9W9; EMBL:AL031536; NID:e1319499
 A: Experimental source: strain 972h(-)
 R: Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
 A: Reference number: T21816
 A: Accession: T39791
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 129-244 <SE2>
 A: Note: intron positions not resolved (incomplete sequence)

Query Match 32.3% Score 47.5; DB 2; Length 244;
 Best Local Similarity 45.8%; Pred. No. 22;
 Matches 11; Conservative 4; Mismatches 6; Indels 3; Gaps 1;

Q9 3 TSSSTKTKQLQHLLLDQMLIN 26
 Db 59 TSEBQKK--ELETHMQSLEMIN 79

RESULT 30
 P86548
 polymorphic outer membrane protein E family [imported] - Chlamydophila pneumoniae (strain

C: Species: Chlamydophila pneumoniae, Chlamydophila pneumoniae
 C: Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C: Accession: F86548
 R: Shirai, M.; Hirakawa, H.; Kimoto, M.; Kishi, F.; Ouchi, K.; Shiba, T.; It
 C: Nucleic Acids Res. 28, 2311-2314, 2000
 A: Title: Comparison of whole genome sequences of chlamydophila pneumoniae J138.
 A: Reference number: A86491; MUID:20330349; PMID:10871362
 A: Accession: F86548
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1-938 <STO>
 A: Cross-references: UNIPROT:Q9Z883; GB:BA000008; NID:gi8978836; PIDN:BA000008; PMID:989772.1; GSPDB:GN
 A: Experimental source: strain J138
 C: Genetics:
 A: Gene: pmp_15
 A: Cross-references: UNIPROT:Q9Z883; GB:BA0001363; NID:gi4376750; PIDN:AA001363
 C: Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C: Accession: H72074; E81593
 R: Kalman, S.; Mitchell, W.; Marth, R.; Lammel, C.; Pan, J.; Olinger, L.; Grimwood, J.;
 Nature Genet. 21, 385-389, 1999
 A: Title: Comparative genomes of Chlamydophila pneumoniae and C. trachomatis.
 A: Reference number: A72000; MUID:9206606; PMID:1092388
 A: Molecule type: DNA
 A: Residues: 1-38 <ARN>
 A: Cross-references: UNIPROT:Q9Z883; GB:BA0001631; NID:gi4376750; PIDN:AA001631
 C: Species: Chlamydophila pneumoniae, Chlamydophila pneumoniae (strain
 C: Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C: Accession: H72074; E81593
 R: Read, T.D.; Brumham, S.R.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McCarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
 A: Title: Genome sequences of Chlamydophila trachomatis MoPn and Chlamydophila pneumoniae AR39.
 A: Reference number: A81500; MUID:2015025; PMID:10684935
 A: Accession: E81593
 A: Molecule type: DNA
 A: Residues: 1-38 <REAA>
 A: Cross-references: GB:AB002190; PIDN:97189209; PMID:97189209; PIDN:AFF38143.1; PMID:9718921
 A: Experimental source: strain AR39, HL cells
 C: Genetics:
 A: Gene: pmp_15; CP0286

RESULT 32
 H82447
 DNA-binding response regulator VCA0532 [imported] - Vibrio cholerae (strain N16961 serog
 C: Species: Vibrio cholerae
 C: Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C: Accession: H82447
 R: Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 chardson, D.; Ermakova, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A: Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A; Reference number: AE2035; MUID:20406833; PMID:10952301

A; Accession: H82447

A; Status: Preliminary

A; Molecule type: DNA

A; Residues: 1-230 <HEI>

A; Cross-references: UNIPROT:Q9KMS6; GB:AE004384; GB:AE003853; NID:g9657936; PIDN:AAF9643

A; Experimental source: serogroup 01; strain N16961; biotype B1 Tor

C; Generics:

A; Gene: VC0532

A; Map position: 2

C; Superfamily: ompR protein; response regulator homology

Query Match 32.0%; Score 47; DB 2; Length 230;

Best Local Similarity 42.9%; Pred. No. 24;

Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 APSSSTKTKTQLOLEHLLQLMNG 21

Db 122 APSTESVEQTRFELGDLVLDL 142

RESULT 33

B70209

conserved hypothetical protein BBA18 - Lyme disease spirochete plasmid A;lp54

C;Species: *Borrelia burgdorferi* (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004

C;Accession: B70209

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, S.; Peterkin, J.; Keravage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, J.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. *Nature* 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.

A;Reference number: A70100; MUID:98065944; PMID:9403685

A;Status: Preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-398 <KLE>

A;Cross-references: UNIPROT:O50911; GB:AE00790; NID:g2690224; PIDN: AAC66245.1; PID:9269

A;Experimental source: strain B31

C;Generics:

A; Genome: Plasmid

C;Superfamily: Lyme disease spirochete plasmid conserved hypothetical protein BBG06

Query Match 32.0%; Score 47; DB 2; Length 398;

Best Local Similarity 40.7%; Pred. No. 45;

Matches 11; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 3 TSSSTKTKTQLOLEHLLQLMNGIN 29

Db 11 TTKRKVKTCTMNFQNLIVLSTINFIN 37

RESULT 34

F89839

hypothetical protein SA0640 [imported] - *Staphylococcus aureus* (strain N315)

C;Species: *Staphylococcus aureus*

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: F89839

R;Kuroda, M.; Ochiai, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani, U.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. *Lancet* 357, 1225-1240, 2001

A;Title: Whole genome sequencing of mettillin-resistant *Staphylococcus aureus*.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: F89839

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 1-557 <KUR>

A;Cross-references: UNIPROT:Q9YVT6; GB:BA000018; PID:g13700576; PIDN: BAB41873.1; GSDB:G

A;Experimental source: strain N315

C;Generics:

A; Gene: SA0640

R;Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
Submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15420

A;Accession: T05656
A;Molecule type: DNA
A;Residues: 1-159 <BEV>
A;Cross-references: UNIPROT:Q9SVE7; EMBL:AL035539
A;Experimental source: cultivar Columbia; BAC clone F22I13
C;Genetics:
A;Map position: 4
A;Introns: 117/1
A;Note: F22I13.50
C;Superfamily: Arabidopsis thaliana hypothetical protein F22I13.50

Query Match 31.6%; Score 46.5; DB 2; Length 159;
Best Local Similarity 46.4%; Pred. No. 19;
Matches 13; Conservative 3; Mismatches 9; Indels 3; Gaps 1;

Qy 2 PTSSSTKTKTQLOLEHLLLDQMLNGIN 29
Db 83 PTPTSHK--LDWEEVYHLQMLNKLN 107

RESULT 38
C84888
hypothetical protein At2g45250 [Imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: C84888
R;Lin, X.; Kaul, S.; Rounsbury, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Reference number: A84420; PMID:20083487; PMID:10617197
A;Accession: C84888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-211 <STO>
A;Cross-references: UNIPROT:O22147; GB:AE002093; NID:g2583136; PIDN:AA82645.1; GSPDB:GN
C;Genetics:
A;Gene: At2g45250
A;Map position: 2
C;Superfamily: Arabidopsis thaliana hypothetical protein F22I13.50

Query Match 31.6%; Score 46.5; DB 2; Length 211;
Best Local Similarity 46.4%; Pred. No. 26;
Matches 13; Conservative 3; Mismatches 9; Indels 3; Gaps 1;

Qy 2 PTSSSTKTKTQLOLEHLLLDQMLNGIN 29
Db 117 PTPTSHK--LDWEEVYHLQMLNKLN 141

RESULT 39
A71946
hypothetical protein jhp0321 - *Helicobacter pylori* (strain J99)
C;Species: *Helicobacter pylori*
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: A71946
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Mertzberg, D.; Miller, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.P.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; PMID:99120557; PMID:9923682
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-293 <ARN>
A;Cross-references: UNIPROT:Q9ZMA1; GB:AE001468; GB:AE001439; NID:g4154838; PIDN:AA0591
C;Genetics:

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OM protein - protein search, using SW model

Run on: September 23, 2005, 12:39:59 ; Search time 52.8525 Seconds

(without alignments)

300.354 Million cell updates/sec

Perfect score: 152

Sequence: 1 MAPSSSTKTKTQLEHLLDQMLINGINN 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 Seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03_*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	96.7	150	2 Q9C001	Q9C001 homo sapien
2	147	96.7	153	1 IL2_HUMAN	P60568 homo sapien
3	147	96.7	153	1 IL2_HYLIA	P60569 hylobates 1
4	147	96.7	153	2 Q6WZ93	Q6WZ93 homo sapien
5	147	96.7	154	1 IL2_MACPA	Q29615 maceca fasc
6	147	96.7	154	1 IL2_MACMU	P68291 macaca mula
7	147	96.7	154	1 IL2_MACNE	P68290 macaca nem
8	147	96.7	154	1 IL2_PAPAN	Q965Y1 papio anub
9	145	95.4	154	1 IL2_SAISC	Q8mkh2 saimiri sci
10	145	95.4	154	2 Q7JFM2	Q7JFM2 aotus lemur
11	145	95.4	154	2 Q7JFM3	Q7JFM3 aotus nigri
12	145	95.4	154	2 Q7JFM4	Q7JFM4 aotus vocif
13	145	95.4	154	2 Q7JFM5	Q7JFM5 aotus nancy
14	145	95.4	154	2 Q9AS38	Q9AS38 papio hamad
15	143	94.1	133	2 Q6QWN0	Q6QWN0 homo sapien
16	143	94.1	133	2 Q7ZTM3	Q7ZTM3 homo sapien
17	142	93.4	154	1 IL2_CERTO	P46649 cercopithecus
18	137	90.1	153	2 Q6N791	Q6N791 homo sapien
19	135.5	89.1	156	2 Q13169	Q13169 homo sapien
20	134	88.2	139	2 Q16334	Q16334 homo sapien
21	116	76.3	154	1 IL2_MIRAN	Q62641 mirounga an
22	114	75.0	154	1 IL2_FELCHA	Q07885 felis silve
23	108.5	71.4	155	2 Q9X783	Q9X783 halichoerus
24	107.5	70.7	66	2 Q9BG74	Q9bg74 canis famili
25	107	70.7	155	1 IL2_CANPA	Q29416 canis famili
26	107	70.4	79	2 Q9TV12	Q9tv12 canis famili
27	107	70.4	152	2 Q8OK33	Q80xg3 peromyscus
28	107	70.4	153	1 IL2_RABBIT	Q77620 oryctolagus
29	106	69.7	133	2 Q9m7R9	Q9m7R9 oryctolagus
30	106	69.7	155	2 Q923T2	Q923T2 sigmoidon hi
31	103	67.8	138	2 Q70329	Q70329 mesocricetus

ALIGNMENTS

RESULT 1

Q9C001 PRELIMINARY; PRT; 150 AA.

ID Q9C001; ID Q9C001; PRELIMINARY; PRT; 150 AA.

AC OC001; AC OC001; PRELIMINARY; PRT; 150 AA.

DT 01-JUN-2001 (TREMBLrel. 17, Created) DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DB Interleukin-2 (Fragment)

OS Homo sapiens (Human)

OU Europa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; NCBI_TaxID=9606;

[1] RN SEQUENCE FROM N.A.

RX MEDLINE=20545237; PubMed=11093171; RX MEDLINE=20545237; PubMed=11093171;

RX Matseanz P., Delgado C., Fresno M., Alcina A.; RT "Allelic selection of human IL-2 gene." RT "Allelic selection of human IL-2 gene.";

RX RL EmbL; AF228636; AAG33575.1; -.

DR HSSP; P60568; 1IRL.

DR GO; GO:0005134; F:extracellular; IBA.

GO; GO:0006955; P:immune response; IBA.

InterPro; IPR00779; 4 helix cytokine.

InterPro; IPR000779; Interleukin-2.

PFAM; PF00715; IL2; 1.

PRINMS; PR00265; INTERLEUKIN2.

ProDom; P003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

DR PROSITE; PS00444; INTERLEUKIN_2; 1.

NON_TER FT 150 150

SQ SEQUENCE 150 AA; 17312 MW; BP25860F8436ACBS CRC64;

Query Match 96.7%; Score 147; DB 2; Length 150; Best Local Similarity 100.0%; Pred. No. 8.5e-14; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APTSSATKTKTQLQLEHLLDQMLINGINN 31

Db 21 APTSSATKTKTQLQLEHLLDQMLINGINN 50

RESULT 2

IL2_HUMAN

ID IL2_HUMAN STANDARD; PRT; 153 AA.

AC P60568; P01595; AC P60568; P01595;

DT 21-JUL-1986 (Rel. 01, Created) DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF) DE (Aldesleukin).

GN Name-IL2;

OS Homo sapiens (Human)

OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;

RN SEQUENCE FROM N.A.

RX MEDLINE=81247753; PubMed=6330695; RX MEDLINE=81247753; PubMed=6330695;

RX Holdbrook N.J., Lieber M., Crabtree G.R.; RT "DNA sequence of the 5' flanking region of the human interleukin 2 gene: homologies with adult T-cell leukemia virus."; RT Nucleic Acids Res. 12:5005-5013 (1984).

RX RN SEQUENCE FROM N.A.

RX MEDLINE=83167472; PubMed=6403867; RX MEDLINE=83167472; PubMed=6403867;

RX Taniguchi T., Matsui H., Fujita T., Takaoka C., Kashima N., Yoshimoto R., Hamuro J.; RT "Structure and expression of a cloned cDNA for human interleukin-2."; RT Nature 302:305-310 (1983).

[3]

RT	and mouse cDNA sequences.";	CC	proliferation and other activities crucial to regulation of the
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	CC	immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.
RN	[11]	CC	- SUBCELLULAR LOCATION: Secreted.
RP	SEQUENCE OF 21-153 FROM N.A.	CC	- - SUBCELLULAR LOCATION: Involved in a form of T-cell acute lymphoblastic leukemia (T-ALL) by a chromosomal translocation t(4;16)(q26;p13) which involves TNFRSF17 and IL2.
RX	MEDLINE=89062420; PubMed=3264184;	CC	- PHARMACEUTICAL: Available under the name Proleukin (Chiron). Used in patients with renal cell carcinoma or metastatic melanoma.
RA	Weir M.P., Chaplin M.A., Wallace D.M., Dykes C.W., Hobden A.N.;	CC	- - SIMILARITY: Belongs to the IL-2 family.
RT	"Structure-activity relationships of recombinant human interleukin 2";	CC	- - DATABASE: NAME=Red Systems, cytokine source book: IL2; WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=206".
RL	Biochemistry 27:6883-6892 (1988).	CC	- -
RN	[12]	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RP	SEQUENCE OF 1-69 FROM N.A.	CC	- -
RX	MEDLINE=87064618; PubMed=3491296;	CC	- -
RA	Siebenlist U., Durand D.B., Bressler P., Holbrook N.J., Norris C.A., Kamoun M., Kant J.A., Crabtree G.R.;	CC	- -
RT	"Promoter region of interleukin-2 gene undergoes chromatin structure changes and confers inducibility on chloramphenicol acetyltransferase gene during activation of T cells";	CC	- -
RL	Mol. Cell. Biol. 6:3042-3049 (1986).	CC	- -
RN	[13]	CC	- -
RP	SEQUENCE OF 1-68 FROM N.A.	CC	- -
RA	Nishino N., Obara K., Maeda S., Shimada K., Onoue K.;	CC	- -
RT	"Organization of the DNA regions flanking the human interleukin 2 gene.";	CC	- -
RL	Biomed. Res. 6:197-205 (1985).	CC	- -
RN	[14]	CC	- -
RP	SEQUENCE OF 21-153, DISULFIDE BOND, AND CARBOHYDRATE-LINKAGE SITE.	CC	- -
RX	MEDLINE=85038540; PubMed=633684;	CC	- -
RA	Robb R.J., Kutny R.M., Panico M., Morris H.R., Chowdhry V.;	CC	- -
RT	"Amino acid sequence and post-translational modification of human interleukin 2.";	CC	- -
RL	Proc. Natl. Acad. Sci. U.S.A. 81:6486-6490 (1984).	CC	- -
RN	[15]	CC	- -
RP	CARBOHYDRATE-LINKAGE SITE.	CC	- -
RX	MEDLINE=90008901; PubMed=2293860;	CC	- -
RA	Conradt H.S., Nintz M., Dittmar K.E.J., Lindemann W., Hoppe J., Hauser H.;	CC	- -
RT	"Expression of human interleukin-2 in recombinant baby hamster kidney, RT Ick-, and Chinese hamster ovary cells. Structure of O-linked carbohydrate chains and their location within the polypeptide.";	CC	- -
RT	RT Ick-, and Chinese hamster ovary cells. Structure of O-linked carbohydrate chains and their location within the polypeptide.";	CC	- -
RL	J. Biol. Chem. 264:17368-17373 (1989).	CC	- -
RN	[16]	CC	- -
RP	X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).	CC	- -
RX	MEDLINE=88070646; PubMed=300515;	CC	- -
RA	Brandhuber B.J., Boone T., Kenney W.C., McKay D.B.;	CC	- -
RT	"Three-dimensional structure of interleukin-2";	CC	- -
RL	Science 238:1707-1709 (1987).	CC	- -
RN	[17]	CC	- -
RP	COMPARISON OF X-RAY STRUCTURES.	CC	- -
RX	MEDLINE=92335891; PubMed=1631562;	CC	- -
RA	Bazan J.F.;	CC	- -
RT	"Unraveling the structure of IL-2.";	CC	- -
RL	Science 257:410-412 (1992).	CC	- -
RN	[18]	CC	- -
RP	RESPONSE TO ABOVE LETTER.	CC	- -
RA	McKay D.B.;	CC	- -
RT	Science 257:412-413 (1992).	CC	- -
RN	[19]	CC	- -
RP	STRUCTURE BY NMR.	CC	- -
RX	MEDLINE=92379010; PubMed=1510960;	CC	- -
RA	Mott H.R., Driscoll P.C., Boyd J., Cooke R.M., Weir M.P.;	CC	- -
RA	Campbell I.D.;	CC	- -
RT	"Secondary structure of human interleukin 2 from 3D heteronuclear NMR experiments";	CC	- -
RL	Biochemistry 31:741-744 (1992).	CC	- -
RN	[20]	CC	- -
RP	3D-STRUCTURE MODELING.	CC	- -
RX	MEDLINE=95111955; PubMed=7529123;	CC	- -
RA	Bamborough P., Hedgecock C.J., Richards W.G.;	CC	- -
RT	"The interleukin-2 and interleukin-4 receptors studied by molecular modelling.";	CC	- -
RL	Structure 2:839-851 (1994).	CC	- -
CC	"- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC	- -

CC	EMBL; M11144; AA035454.1; -.	DR	InterPro; IPR000779; Interleukin-2.
DR	PTB; AA04067; ICG32.	DR	PFam; PF00715; IL2; 1.
DR	InterPro; IPR000779; Interleukin-2.	DR	PRINTS; PR00265; INTERLEUKIN2.
DR	PRINT; PR00715; IL2; 1.	DR	ProDom; PR003649; Interleukin-2; 1.
DR	PRINTS; PR00265; INTERLEUKIN2.	DR	SMART; SM00189; IL2; 1.
DR	ProDom; PD003649; Interleukin-2; 1.	DR	PROSITE; PS00422; INTERLEUKIN-2; 1.
DR	SMART; SM00189; IL2; 1.	SQ	SEQUENCE 153 AA; 17597 MW; -1942F50F25960E88 CRC64;
DR	PROSITE; PS00424; INTERLEUKIN 2; 1.	Query Match	96.7%; Score 147; DB 2; Length 153;
KW	cytokine; Glycoprotein; Growth factor; Immune response; Signal;	Best Local Similarity	100.0%; Pred. No. 8.7e-14;
T-CELL	By similarity.	Matches	30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT	Interleukin-2.	Qy	2 APTSSSTKTKTQLEHILLDQMINLINGINN 31
FT	CHAIN 21 153 23 O-linked (GalNAc. . .) (By similarity).	Db	21 APTSSSTKTKTQLEHILLDQMINLINGINN 50
FT	CARBOHYD 23 78 125 By similarity.		
FT	DISULFD 78 153 AA; 17628 MW; 59E2F0F25860F84 CRC64;		
SQ	RESULT 5		
Query Match	96.7%; Score 147; DB 1; Length 153;	IL2_MACFA	STANDARD;
Best Local Similarity	100.0%; Pred. No. 8.7e-14;	ID	IL2_MACFA
Matches	30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AC	Q297515;
Qy	2 APTSSSTKTKTQLEHILLDQMINLINGINN 31	AC	Q297515;
Db	21 APTSSSTKTKTQLEHILLDQMINLINGINN 50	DT	01-NOV-1997 (Rel. 35, Created)
		DT	01-NOV-1997 (Rel. 35, Last sequence update)
		DT	05-JUL-2004 (Rel. 44, Last annotation update)
		DB	Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGP) .
		GN	Name=IL2;
		OS	Macaca fasciularis (Crab eating macaque) (Cynomolgus monkey).
		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
		OC	Cercopithecinae; Macaca.
		NCBI_TaxId	9541;
		RN	SEQUENCE FROM N.A.
		RC	TISSUE=Peripheral blood;
		RA	Submitted (JUDY-1995) to the EMBL/GenBank/DBJ databases.
		RL	-i- FUNCTION: Produced by T-cells in response to antigenic or
		CC	mitogenic stimulation, this protein is required for T-cell
		CC	proliferation and other activities crucial to regulation of the
		CC	immune response. Can stimulate B cells, monocytes, lymphokine-
		CC	activated killer cells, natural killer cells, and glioma cells (By
		CC	similarity).
		CC	-i- SUBCELLULAR LOCATION: Secreted.
		CC	-i- SIMILARITY: Belongs to the IL-2 family.
		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
		CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
		CC	the European Bioinformatics Institute. There are no restrictions on its
		CC	use by non-profit institutions as long as its content is in no way
		CC	modified and this statement is not removed. Usage by and for commercial
		CC	entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
		CC	-i- TISSUE/PCR rescued clones;
		CC	RESEQUENCE FROM N.A.
		CC	RESEQUENCE PCR rescued clones; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
		CC	Altschul S.F., Feingold E.A., Grouse L.H., Degege J.G., Schuler G.D.,
		RA	Klauser R.D., Collins F.S., Wagner L., Shemesh C.M., Bhat N.K.,
		RA	Altshul S.F., Zeeberg B.R., Bueck W.H., Schaefer C.F., Bhat N.K.,
		RA	Diatchenko L., Marusina A.K., Farmer A.A., Rubin G.M., Hong L.,
		RA	Stapleton M., Soares M.B., Bonaldo M.P., Csanav T.L., Cheneet T.E.,
		RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
		RA	Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
		RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
		RA	Richards D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
		RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
		RA	Whiting M., Madan A., Young A.M., Shevchenko Y., Bouffard G.G.,
		RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
		RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N., Butterfield Y.S.,
		RA	Krzywinski M.I., Skalska U., Smailus D.E., Schenck J.E.,
		RA	Jones S.J., Marra M.A.,
		RT	"Generation and initial analysis of more than 15,000 full-length human
		RT	and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16689-16903 (2002).
		RL	[2]
		RN	SEQUENCE FROM N.A.
		RC	TISSUE/PCR rescued clones;
		RA	Strausberg R.; Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
		DR	EMBL; BC066254; AAH66254.1; -.
		DR	GO; GO:0005776; C: extracellular; IEA.
		DR	GO; GO:005134; P: interleukin-2 receptor binding; IEA.
		DR	GO; GO:0005955; P: immune response; IEA.
		DR	InterPro; IPR009079; 4_helix_cytokine.
		Query Match	96.7%; Score 147; DB 1; Length 154;
		Best Local Similarity	100.0%; Pred. No. 8.8e-14;
		Matches	30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6	
Qy	2 APTSSSTKTKTQLEHLLDQMLINGINN 31 ID_2_MACMU ID_2_MACMU; STANDARD; P68791; P51498; AC 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update)
Db	21 APTSSSTKTKTQLEHLLDQMLINGINN 50 DT 25-OCT-2004 (Rel. 45, Last annotation update) Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
Qy	Name=IL2; Macaca mulatta (Rhebus macaque). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Cercopitheciidae; Cercopitheciinae; Macaca. NCBI_Taxid=9544; RN [1] SEQUENCE FROM N.A. TISSUE=Blood; MEDLINE=96003435; PubMed=7561102; Villinger F.J., Brar S.S., Mayne A.B., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and nonhuman primates."; J. Immunol. 155:33946-33954 (1995).
Db	-I- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine- activated killer cells, natural killer cells, and glioma cells (By similarity). -I- SUBCELLULAR LOCATION: Secreted. -I- SIMILARITY: Belongs to the IL-2 family.
Qy	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). CC CC DR EMBL; U19847; AAB60400.1; -. CC DR HSSP; P01585; IM48. CC DR InterPro; IPR009079; 4-helix_cytokine. CC DR InterPro; IPR000779; Interleukin-2. CC DR Pfam; PF00715; IL2; 1. CC DR PRINTS; PRO0265; INTERLEUKIN2. CC DR SMART; SM00189; IL2; 1. CC DR PROSITE; PS00424; INTERLEUKIN_2; 1. CC DR CYCDB; Glycoprotein; Growth factor; Immune response; Signal; KW T-cell. CC FT SIGNAL. 1 20 By similarity. CC FT CHAIN. 21 154 Interleukin-2. CC FT CARBOHYD. 23 23 O-linked (GalNAc. . .) (By similarity). CC FT DISULFID. 78 126 By similarity. CC SQ SEQUENCE 154 AA; 17685 MW; 64EBA80F204BA49 CRC64;
Db	CC DR EMBL; U19847; AAB60400.1; -. CC DR HSSP; P01585; IM48. CC DR InterPro; IPR009079; 4-helix_cytokine. CC DR InterPro; IPR000779; Interleukin-2. CC DR Pfam; PF00715; IL2; 1. CC DR PRINTS; PRO0265; INTERLEUKIN2. CC DR SMART; SM00189; IL2; 1. CC DR PROSITE; PS00424; INTERLEUKIN_2; 1. CC DR CYCDB; Glycoprotein; Growth factor; Immune response; Signal; KW T-cell. CC FT SIGNAL. 1 20 By similarity. CC FT CHAIN. 21 154 Interleukin-2. CC FT CARBOHYD. 23 23 O-linked (GalNAc. . .) (By similarity). CC FT DISULFID. 78 126 By similarity. CC SQ SEQUENCE 154 AA; 17685 MW; 64EBA80F204BA49 CRC64;
Qy	Query Match 96.7%; Score 147; DB 1; Length 154; Best Local Similarity 100.0%; Pred. No. 8.8e-14; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	Qy 2 APTSSSTKTKTQLEHLLDQMLINGINN 31 ID_2_MACNE ID_2_MACNE; STANDARD; PRT; 154 AA.
Qy	2 APTSSSTKTKTQLEHLLDQMLINGINN 31 ID_2_MACNE ID_2_MACNE; STANDARD; PRT; 154 AA.
Db	Db 21 APTSSSTKTKTQLEHLLDQMLINGINN 50 Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
RESULT 7	
Qy	2 APTSSSTKTKTQLEHLLDQMLINGINN 31 ID_2_MACNE ID_2_MACNE; STANDARD; PRT; 154 AA.
Db	Db 21 APTSSSTKTKTQLEHLLDQMLINGINN 50 Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).

Qy	SQ	SEQUENCE	154 AA;	17675 MW;	AB752ABBADA96469 CRC64;
Db	21	APTSSTKCTQLEHLLDQMLINGINN 50			
RESULT 11					
Qy 2 APTSSTKCTQLEHLLDQMLINGINN 31					
Q7JFM3	Q7JFM3	PRELIMINARY;	PRT;	154 AA.	
AC	Q7JFM3;				
DR	05-JUL-2004	(TREMBLrel. 27, Created)			
DR	05-JUL-2004	(TREMBLrel. 27, Last sequence update)			
DR	05-JUL-2004	(TREMBLrel. 27, Last annotation update)			
OS	Aotus nigriceps	(Black-headed owl monkey).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.				
NCBI_TaxID	57175;				
RN					
RP	SEQUENCE FROM N.A.				
RA	Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A., Patarroyo M.E.,				
RA	Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.				
DR	U88363; AA01536; 1.				
DR	GO; GO:0005576; C: extracellular.				
DR	GO; GO:0005134; F: interleukin-2 receptor binding; IEA.				
DR	GO; GO:0006955; P: immune response; IEA.				
DR	GO; GO:0006955; P: immune response; IEA.				
DR	InterPro; IPR009079; 4 helix cytokine.				
DR	InterPro; IPR009079; 4 helix cytokine.				
DR	InterPro; IPR009079; Interleukin-2.				
DR	PRINTS; PR00265; INTERLEUKIN2.				
DR	PRODom; PD003649; Interleukin-2.				
DR	SMART; SM00189; IL2; 1.				
DR	PROSITE; PS00424; INTERLEUKIN-2; 1.				
SQ	SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;				
Query Match 95.4%; Score 145; DB 2; Length 154;					
Best Local Similarity 96.7%; Pred. No. 1.8e-13; Mismatches 1; Indels 0; Gaps 0;					
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;					
Qy 2 APTESSSTKCTQLEHLLDQMLINGINN 31					
Q7JFM4	Q7JFM4	PRELIMINARY;	PRT;	154 AA.	
AC	Q7JFM4;				
DR	05-JUL-2004	(TREMBLrel. 27, Created)			
DR	05-JUL-2004	(TREMBLrel. 27, Last sequence update)			
DR	05-JUL-2004	(TREMBLrel. 27, Last annotation update)			
OS	Aotus vociferans (Spix's owl monkey).				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.				
NCBI_TaxID	57176;				
RN					
RP	SEQUENCE FROM N.A.				
RA	Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A., Patarroyo M.E.,				
RA	Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.				
DR	U88362; AA01537; 1.				
DR	GO; GO:0005576; C: extracellular.				
DR	GO; GO:0006955; B: immune response; IEA.				
DR	InterPro; IPR009079; 4 helix cytokine.				
DR	PRINTS; PR00265; INTERLEUKIN2.				
DR	PRODom; PD003649; Interleukin-2.				
DR	SMART; SM00189; IL2; 1.				
DR	PROSITE; PS00424; INTERLEUKIN-2; 1.				
SQ	SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;				
Query Match 95.4%; Score 145; DB 2; Length 154;					
Best Local Similarity 96.7%; Pred. No. 1.8e-13; Mismatches 1; Indels 0; Gaps 0;					
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;					
Qy 2 APTESSSTKCTQLEHLLDQMLINGINN 50					
Q7JFM4	Q7JFM4	PRELIMINARY;	PRT;	154 AA.	
AC	Q7JFM4;				
DR	05-JUL-2004	(TREMBLrel. 27, Created)			
DR	05-JUL-2004	(TREMBLrel. 27, Last sequence update)			
DR	05-JUL-2004	(TREMBLrel. 27, Last annotation update)			
OS	Aotus vociferans (Spix's owl monkey).				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cebidae; Aotinae; Aotus.				
NCBI_TaxID	57175;				
RN					
RP	SEQUENCE FROM N.A.				
RA	Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A., Patarroyo M.E.,				
RA	Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.				
DR	U88365; AA01538; 1.				
DR	GO; GO:0005576; C: extracellular.				
DR	GO; GO:0006955; B: immune response; IEA.				
DR	InterPro; IPR009079; 4 helix cytokine.				
DR	PRINTS; PR00265; INTERLEUKIN2.				
DR	PRODom; PD003649; Interleukin-2.				
DR	SMART; SM00189; IL2; 1.				
DR	PROSITE; PS00424; INTERLEUKIN-2; 1.				
SQ	SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;				
Query Match 95.4%; Score 145; DB 2; Length 154;					
Best Local Similarity 96.7%; Pred. No. 1.8e-13; Mismatches 1; Indels 0; Gaps 0;					
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;					
Qy 2 APTESSSTKCTQLEHLLDQMLINGINN 31					
Q9XS38	Q9XS38	PRELIMINARY;	PRT;	154 AA.	
AC	Q9XS38;				
DR	01-NOV-1999	(TREMBLrel. 12, Created)			
DR	01-NOV-1999	(TREMBLrel. 12, Last sequence update)			
DR	01-MAR-2004	(TREMBLrel. 26, Last annotation update)			
DE	IL2.				
OS	papio hamadryas (Hamadryas baboon).				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cercopithecidae; Cercopithecinae; Papio.				
NCBI_TaxID	9557;				
RN					
RP	SEQUENCE FROM N.A.				
RA	Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A., Patarroyo M.E.,				
RA	Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.				
DR	U88365; AA01538; 1.				
DR	HSSP; P60568; 1IRL.				
DR	GO; GO:0005576; C: extracellular.				
DR	GO; GO:0005134; F: interleukin-2 receptor binding; IEA.				
DR	GO; GO:0006955; B: immune response; IEA.				
DR	InterPro; IPR009079; 4 helix cytokine.				
DR	PRINTS; PR00265; INTERLEUKIN2.				
DR	PRODom; PD003649; Interleukin-2.				
DR	SMART; SM00189; IL2; 1.				
DR	PROSITE; PS00424; INTERLEUKIN-2; 1.				
SQ	SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;				
Query Match 95.4%; Score 145; DB 2; Length 154;					
Best Local Similarity 96.7%; Pred. No. 1.8e-13; Mismatches 1; Indels 0; Gaps 0;					
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;					

DR	InterPro; IPR009079; 4_helix_cytokine.	DR	HSSP; P60568; 1IRL.
DR	Pfam; PF00715; IL2; 1.	GO	GO:000576; C: extracellular; IEA.
DR	PRINTS; PR00265; INTERLEUKIN2.	DR	GO; GO:005134; P: interleukin-2 receptor binding; IEA.
DR	SMART; SM003649; Interleukin-2; 1.	DR	GO; GO:005955; P: immune response; IEA.
DR	PROSITE; PS00424; INTERLEUKIN_2; 1.	DR	InterPro; IPR009079; 4_helix_cytokine.
DR	SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;	DR	InterPro; IPR000779; Interleukin-2.
Qy	Query Match 95.4%; Score 145; DB 2; Length 154; Best Local Similarity 96.7%; Pred. No. 1.8e-13; Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	DR	Pfam; PF00715; IL2; 1.
Db	2 APTSSSTKTKTQLEHHLLDQMLNGINN 31 21 APSSSTKTKTQLEHHLLDQMLNGINN 50	DR	ProdB; P0003649; Interleukin-2; 1.
RESULT 15		DR	SMART; SM00189; IL2; 1.
QDQWNO	PRELIMINARY; PRT; 133 AA.	DR	PROSITE; PS00424; INTERLEUKIN_2; 1.
AC	GOQWNO;	DR	SEQUENCE 133 AA; 15461 MW; 1699PEA880959B90 CRC64;
DT	05-JUL-2004 (TREMBLrel. 27, Created)	ID	Best Local Similarity 100.0%; Pred. No. 3e-13; Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	STANDARD	Score 143; DB 2; Length 133;
DB	Interleukin-2.	PRT	94.1%; Pred. No. 3e-13; Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OS	Homo sapiens (Human).	SEQUENCE	133 AA; 15461 MW; 1699PEA880959B90 CRC64;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.	Qy	3 PTSSSTKTKTQLEHHLLDQMLNGINN 31
OX	NCBI_TaxID=9606; [1]	Db	2 PTSSSTKTKTQLEHHLLDQMLNGINN 30
RN	SEQUENCE FROM N.A.	RESULT 17	
RA	Chikara, S.K.; Sharma, G.; Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.	ID	IL2_CERTO
RL	DRB23040; AY317753.1.	AC	P46449;
DR	GO; GO:0005576; C: extracellular; IEA.	DT	01-NOV-1995 (Rel. 32, Created)
DR	GO; GO:005134; P: interleukin-2 receptor binding; IEA.	DT	01-NOV-1995 (Rel. 32, Last sequence update)
DR	GO; GO:006355; P: immune response; IEA.	DT	05-JUL-2004 (Rel. 44, Last annotation update)
DR	InterPro; IPR009079; 4_helix_Cytokine.	DB	Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
DR	InterPro; IPR00715; IL2; 1.	DN	Name=IL2;
DR	PROSITE; PS00424; INTERLEUKIN_2; 1.	OS	Cercocetus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
DR	SMART; SM00189; IL2; 1.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Cercopitheciidae; Cercopithecinae; Cercopithecidae;
DR	PROSITE; PS00265; INTERLEUKIN2.	OC	Mammalia; Eutheria; Primates; Catarhini; Cercopitheciidae;
DR	PRINTS; PR00265; INTERLEUKIN2.	OC	Cercopithecinae; Cercopithecidae;
DR	PRODOM; P0003649; Interleukin-2; 1.	SEQUENCE FROM N.A.	
DR	PROSITE; PS00424; INTERLEUKIN_2; 1.	RN	[1]
DR	SEQUENCE 133 AA; 15462 MW; 1699PEA8809DB3B0 CRC64;	RP	
Qy	Query Match 94.1%; Score 143; DB 2; Length 133; Best Local Similarity 100.0%; Pred. No. 3e-13; Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RC	
Db	3 PTSSSTKTKTQLEHHLLDQMLNGINN 31 2 PTSSSTKTKTQLEHHLLDQMLNGINN 30	TISSUE=Blood;	
RESULT 16		RX	MEDLINE=95003435; PubMed=7561102;
QDZ7M3	PRELIMINARY; PRT; 133 AA.	RA	Villinger, F.J.; Brar, S.S.; Mayne, A.E.; Chikala, N.; Ansari, A.A.;
ID	QDZ7M3	RT	*Comparative sequence analysis of cytokine genes from human and non-human primates.
AC	GOQWNO;	RL	J. Immunol. 155:3946-3954 (1995).
DT	01-OCT-2003 (TREMBLrel. 25, Created)	CC	-1- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)	CC	-1- SUBCELLULAR LOCATION: Secreted.
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	CC	-1- SIMILARITY: Belongs to the IL-2 family.
DE	Interleukin-2.	CC	
OS	Homo sapiens (Human).	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.	CC	
OX	NCBI_TaxID=9606; [1]	CC	
RN	SEQUENCE FROM N.A.	CC	
RA	Chikara, S.K.; Jaiswal, P.; Sharma, G.; Submitted (APR-2003) to the EMBL/Genbank/DDBJ databases.	DR	
RL	AY283686; AAP35033.1; -.	DR	
DR		DR	

FT	DISULFID	78	126	By similarity.
FT	VARIANT	25	25	R -> S.
FT	VARIANT	74	74	K -> E.
SQ	SEQUENCE	154 AA;	17754 MW;	9FEB51814204BA48 CRC64;
Query Match	Best Local Similarity	93.4%	Score 142;	DB 1; Length 154;
Matches	29;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
Qy	2 APTSSSTKTKTQLOLEHLLIDQMLNNGINN 31	RESULT 19	2 APTSSSTKTKTQLOLEHLLIDQMLNNGINN 31	Qy 2 APTSSSTKTKTQLOLEHLLIDQMLNNGINN 31
Db	21 APTSRSTKTKTQLOLEHLLIDQMLNNGINN 50		21 APTSSSTKTKTQLOLEHLLIDQMLNNGINN 50	Db 21 APTSSSTKTKTQLOLEHLLIDQMLNNGINN 50
RESULT 18				
QDN91	SEQUENCE FROM N.A.	PRELIMINARY;	PRT;	153 AA.
AC	QDN91;	RESULT 19	Q13169	PRELIMINARY;
DR	05-JUL-2004 (TREMBLrel. 27, Created)		Q13169	PRT;
DR	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		Q13169	156 AA.
DR	05-JUL-2004 (TREMBLrel. 27, Last annotation update)		Q13169	156 AA.
DB	Interleukin 2.		Q13169	156 AA.
GN	Name=IL2;		Q13169	156 AA.
OS	Homo sapiens (Human).		Q13169	156 AA.
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		Q13169	156 AA.
NCBI TaxID	9606;		Q13169	156 AA.
OX	NCBI TaxID=9606;		Q13169	156 AA.
RN	SEQUENCE FROM N.A.		Q13169	156 AA.
RP	SEQUENCE FROM N.A.		Q13169	156 AA.
RC	TISSUE-PCR rescued clones;		Q13169	156 AA.
RX	MEDLINE:22388257; PubMed:12477932; DOI=10.1073/pnas.242603899;		Q13169	156 AA.
RA	Klausner R.D., Feingold B.A., Grouse L.H., Derge J.G.,		Q13169	156 AA.
RA	Altenschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,		Q13169	156 AA.
RA	Hajkova R.F., Jordahl H., Moore T., Max S.I., Wang F.,		Q13169	156 AA.
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		Q13169	156 AA.
RA	Stapleton M., Soresi M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		Q13169	156 AA.
RA	Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		Q13169	156 AA.
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		Q13169	156 AA.
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		Q13169	156 AA.
RA	Villanueva D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		Q13169	156 AA.
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		Q13169	156 AA.
RA	Whiting M., Madan A., Young B.C., Shevchenko Y., Bouffard G.G.,		Q13169	156 AA.
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		Q13169	156 AA.
RA	Rodríguez A.C., Grimes J., Schmutz J., Myers R.M., Butterfield Y.S.,		Q13169	156 AA.
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schimrich A., Schein J.E.,		Q13169	156 AA.
RA	Jones S.J., Marrs M.A.,		Q13169	156 AA.
RA	"Generation and initial analysis of more than 15,000 full-length human		Q13169	156 AA.
RA	RNA sequences."		Q13169	156 AA.
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		Q13169	156 AA.
RN	SEQUENCE FROM N.A.		Q13169	156 AA.
RP	TISSUE-PCR rescued clones;		Q13169	156 AA.
RA	Strausberg R.		Q13169	156 AA.
DR	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.		Q13169	156 AA.
DR	EMBL; EMBL6356; AAH66356.1		Q13169	156 AA.
DR	GO: GO-0005576; C:extracellular; IEA.		Q13169	156 AA.
DR	GO; GO-0005134; P:interleukin-2 receptor binding; IEA.		Q13169	156 AA.
DR	GO-0006355; P:immune response; IEA.		Q13169	156 AA.
DR	InterPro: IPR009079; 4 helix cytokine.		Q13169	156 AA.
DR	InterPro: IPR00715; IL2; 1.		Q13169	156 AA.
DR	PRINTS: PR00265; INTERLEUKIN2.		Q13169	156 AA.
DR	SMART: SM00349; Interleukin-2.		Q13169	156 AA.
DR	PROSITE: PS00424; INTERLEUKIN-2.		Q13169	156 AA.
DR	PROSITE: PS00424; INTERLEUKIN-2.		Q13169	156 AA.
DR	SEQUENCE 153 AA;		Q13169	156 AA.
Qy	2 APTSSSTKTKTQLOLEHLLIDQMLNNGINN 31	RESULT 20	2 APTSSSTKTKTQLOLEHLLIDQMLNNGINN 31	Qy 2 APTSSSTKTKTQLOLEHLLIDQMLNNGINN 31
Db	21 APTSSSTKTKTQLOLEHLLIDQMLNNGINN 53		21 APTSSSTKTKTQLOLEHLLIDQMLNNGINN 53	Db 21 APTSSSTKTKTQLOLEHLLIDQMLNNGINN 53
RESULT 20				
QDN91	SEQUENCE FROM N.A.	PRELIMINARY;	PRT;	139 AA.
AC	Q16334;	RESULT 20	Q16334;	PRELIMINARY;
DR	01-NOV-1996 (TREMBLrel. 01, Created)		Q16334;	PRT;
DR	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		Q16334;	139 AA.
DR	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		Q16334;	139 AA.
DR	IL-2 protein (Fragment).		Q16334;	139 AA.
GN	Name=IL-2;		Q16334;	139 AA.
OS	Homo sapiens (Human).		Q16334;	139 AA.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		Q16334;	139 AA.
OX	NCBI TaxID=9606;		Q16334;	139 AA.
RN	SEQUENCE FROM N.A.		Q16334;	139 AA.
RP	SEQUENCE FROM N.A.		Q16334;	139 AA.
RA	Best Local Similarity	90.1%	Score 137;	DB 2; Length 153;
RA	Best Local Similarity	96.7%	Score 137;	DB 2; Length 153;
RA	Matches 29;	Conservative	Pred. No. 2.7e-12;	Indels 0; Gaps 0;
RA	Matches 29;	Conservative	Pred. No. 2.7e-12;	Indels 0; Gaps 0;

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PT	CARBOHYD	111	111	N-linked (GlcNAc, ·) (Potential).	RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
PT	CONFLICT	3	4	KI → RM (in Ref. 2).	DR	AF333117; AAK01437.1; -.
PT	CONFLICT	150	150	F → I (in Ref. 2).	DR	HSSP; P60568; 1ILR.
SQ	SEQUENCE	154 AA;	17653 MW;	2E71EBD8B9665BF CRC64;	DR	GO; GO:0005576; C:extracellular; IEA.
Query Match	Best Local Similarity	75.0%	Score 114; DB 1; Length 154;	DR	GO; GO:0005134; F:interleukin-2 receptor binding; IEA.	
Matches	22;	Conservative	5; Mismatches 3; Indels 0; Gaps 0;	DR	GO; GO:0006955; P:immune response; IEA.	
Qy	2 APSSSTKTKTQLEHLLIDQMLINGINN 31			DR	InterPro; IPR009079; 4 helix cytokine.	
Db	21 APSSSTKETQQLEQQLDLRLLNGINN 50			DR	InterPro; IPR000779; Interleukin-2.	
RESULT 23						
Q9XT83	PRELIMINARY;	PRT;	155 AA.	DR	Pfam: PF00715; IL2; 1.	
AC	Q9XT83;			DR	PRINTS; PRO0265; INTERLEUKIN2.	
DT	01-NOV-1999	(TREMBLrel. 12, Created)		DR	PRODOM; PD010369; Interleukin-2; 1.	
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		DR	SMART; SM00189; IL2; 1.	
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		FT	NON-TER 1	
DE	Interleukin 2.			FT	NON-TER 1	
OS	Halichoeres Grypus (Gray seal).			FT	66	
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			SQ	SEQUENCE 66 AA; 7389 MW; 22A893F79DA2AB47 CRC64;	
OC	Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Halichoeridae.					
OX	NCBI_TaxID=9711;					
RN						
RP	SEQUENCE FROM N.A.					
RX	MEDLINE:99221046; PubMed:10206205; DOI=10.1016/S0165-2427(99)00009-4;					
RA	st-Laurent G., Beliveau C., Archambault D.;					
RT	"Molecular cloning and phylogenetic analysis of beluga whale (Delphinapterus leucas) and grey seal (Halichoeretus Grypus) interleukin 2."					
RR	De;					
RU	Vet. Immunol. Immunopathol. 67:185-194 (1999).					
DR	EMBL; AF02871; AFAD048.1; -.					
DR	HSSP; B60568; 1ILR.					
DR	GO; GO:0005576; C:extracellular; IEA.					
DR	GO; GO:005134; F:interleukin-2 receptor binding; IEA.					
DR	GO; GO:0006955; P:immune response; IEA.					
DR	InterPro; IPR009079; 4 helix cytokine.					
DR	PRIM; IPR00715; IL2; 1.					
DR	PRINTS; PRO0265; INTERLEUKIN2.					
DR	PRODOM; PD003649; -.					
DR	SMART; SM00189; IL2; 1.					
DR	PROSITE; PS00424; INTERLEUKIN-2; 1.					
SQ	SEQUENCE 155 AA; 17860 MW; F18P449AC672241A CRC64;					
Query Match	Best Local Similarity	71.4%	Score 108.5; DB 2; Length 155;	RP	SEQUENCE FROM N.A.	
Matches	23;	Conservative	5; Mismatches 2; Indels 1; Gaps 1;	RP	SEQUENCE FROM N.A.	
Qy	2 AP-TSSSTKTKTQLEHLLIDQMLINGINN 31			RP	SEQUENCE FROM N.A.	
Db	21 APSSSTKETQQLEQQLDLRLLNGINN 51			RP	SEQUENCE FROM N.A.	
RESULT 24						
Q9BG74	PRELIMINARY;	PRT;	66 AA.	RP	SEQUENCE FROM N.A.	
AC	Q9BG74;			RP	SEQUENCE FROM N.A.	
DT	01-JUN-2001	(TREMBLrel. 17, Created)		RP	SEQUENCE FROM N.A.	
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)		RP	SEQUENCE FROM N.A.	
DE	Interleukin 2 (Fragment).			RP	SEQUENCE FROM N.A.	
OS	Canis familiaris (Dog).			RP	SEQUENCE FROM N.A.	
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			RP	SEQUENCE FROM N.A.	
OC	Mammalia; Eutheria; Carnivora; Pinnipedia; Canidae.			RP	SEQUENCE FROM N.A.	
OX	NCBI_TaxID=9615;			RP	SEQUENCE FROM N.A.	
RN				RP	SEQUENCE FROM N.A.	
RC	SEQUENCE FROM N.A.			RP	SEQUENCE FROM N.A.	
RC	TISSUE=Blood;			RP	SEQUENCE FROM N.A.	
RA	Markus S., Groene A., Baumgaertner W.;			RP	SEQUENCE FROM N.A.	

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CC EMBL: D30710; BA06378.1; -. DR EMBL: U28141; AA68969.1; -. DR EMBL: U11689; AAAT75360.1; -. DR EMBL: B01585; 3TNC.

DR InterPro: IPR009079; 4 helix_cytokine.

DR InterPro: IPR000779; Interleukin-2.

DR PRINTS: PR00265; INTERLEUKIN2.

DR PRODOM: PD00449; Interleukin-2; 1.

DR SMART: SM00189; IL2; 1.

DR PROSITE: PS00424; INTERLEUKIN_2; 1.

KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal;

KW T-cell; Interleukin-2; -. DR SIGNAL 1 20 By similarity.

FT CHAIN 21 155 Interleukin-2.

FT CARBOHYD 24 24 O-linked (GlcNAc. . .) (By similarity).

FT CARBOHYD 112 112 N-linked (GlcNAc. . .) (Potential).

FT DISULFID 79 127 By similarity.

FT DISULFID 79 127 (Potential).

FT FT 4 4 M -> I (In Ref. 3).

FT CONFLICT 37 37 Q -> R (In Ref. 3).

FT CONFLICT 151 151 F -> Y (In Ref. 3).

FT CONFLICT 154 154 L -> M (In Ref. 3).

FT SEQUENCE 155 AA; 17668 MW; D1235486BF4ACID CRC64;

FT SEQUENCE 155 AA; 17668 MW; D1235486BF4ACID CRC64;

FT SEQUENCE 70.7%; Score 107.5; DB 1; Length 155;

FT Best Local Similarity 70.1%; Pred. No. 7.3e-08; Matches 22; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

FT 2 AP-TSSSTKTKTOLQLEHLLDQMLINGINN 31

FT 21 APITSSSTKETEQMEEQLLDQMLINGVNN 51

DR Q9TV12 PRELIMINARY; PRT; 79 AA.

AC 01-MAY-2000 (TREMBLrel. 13, Created)

DR 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DR 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DR Interleukin-2 (Fragment).

OS Canis familiaris (Dog).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

NCBI_TAXID=9615; RN [1]

RP SEQUENCE FROM N.A.

RA German A.J.; Helps C.R.; Harley R.; Hall E.J.; Day M.J.;

RL EMBL: AF091131; AAD46989.1; -. DR EMBL: AF091131; AAD46989.1; -. DR HSSP: F60568; 1IRL.

DR GO: GO-0005576; C: extracellular; IEA.

DR GO: GO-0005334; F: interleukin-2 receptor binding; IEA.

DR GO: GO-0006955; F: immune response; IEA.

DR InterPro: IPR009079; 4 helix_cytokine.

DR PROSITE: PS00424; INTERLEUKIN_2; 1.

DR PRINTS: PR00265; INTERLEUKIN2.

DR PRODOM: PD00449; Interleukin-2; 1.

DR SMART: SM00189; IL2; 1.

DR PROSITE: PS00424; INTERLEUKIN_2; 1.

FT NON-TER 1 1

FT NON-TER 79 79

FT SEQUENCE 79 AA; 9087 MW; 83079BF8F8A659BD CRC64;

FT SEQUENCE 70.4%; Score 107; DB 2; Length 79;

FT Best Local Similarity 71.4%; Pred. No. 4.1e-08; Matches 6; Mismatches 2; Indels 0; Gaps 0;

FT SEQUENCE 70.4%; Score 107; DB 2; Length 79;

FT Best Local Similarity 71.4%; Pred. No. 4.1e-08; Matches 6; Mismatches 2; Indels 0; Gaps 0;

FT SEQUENCE 70.4%; Score 107; DB 2; Length 79;

FT Best Local Similarity 71.4%; Pred. No. 4.1e-08; Matches 6; Mismatches 2; Indels 0; Gaps 0;

FT SEQUENCE 70.4%; Score 107; DB 2; Length 79;

FT Best Local Similarity 71.4%; Pred. No. 4.1e-08; Matches 6; Mismatches 2; Indels 0; Gaps 0;

FT SEQUENCE 70.4%; Score 107; DB 2; Length 79;

FT Best Local Similarity 71.4%; Pred. No. 4.1e-08; Matches 6; Mismatches 2; Indels 0; Gaps 0;

FT SEQUENCE 70.4%; Score 107; DB 2; Length 79;

FT Best Local Similarity 71.4%; Pred. No. 4.1e-08; Matches 6; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TSSSTKTKTOLQLEHLLDQMLINGINN 31
Db 7 TSSSTKETEQMEEQLLDQMLINGVNN 34

RESULT 27

Q80XG3

PRELIMINARY;

PRT; 152 AA.

ID Q80XG3;

AC Q80XG3;

DT 01-JUN-2003 (TREMBLrel. 24, Created)

DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update).

DB Interleukin-2 (Fragment).

GN Name=IL2;

NCBI_TAXID=1042;

OC Peromyscus.

OC Peromyscus.

NCBI_TAXID=1042;

OX OX.

NCBI_TAXID=1042;

RN RN.

RP SEQUENCE FROM N.A.

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

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RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

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RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

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RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

RA Schountz T.; Buniger A.; Davenport B.; Hegg T.;

CC	immune response. Can stimulate B cells, monocytes, lymphokine
CC	activated killer cells, natural killer cells, and glioma cells.
CC	- - SUBCELLULAR LOCATION: Secreted
CC	- - SIMILARITY: Belongs to the IL-2 family.
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CC	- - EMBL; P0168057; AAC23838.1; - .
CC	DR HSSP; P01585; 1M4A.
CC	DR InterPro; IPR09079; 4_helix_cycokine.
CC	DR InterPro; IPR00779; Interleukin-2.
CC	DR Pfam; PF00715; IL2; 1.
CC	DR PRINTS; PR02655; INTERLEUKIN2.
CC	DR ProDom; P003649; Interleukin-2; 1.
CC	DR SMART; SM00189; IL2; 1.
CC	DR PROSITE; PS00424; INTERLEUKIN2; 1.
CC	KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal; T-cell.
CC	PT SIGNAL 1 20 By similarity.
CC	PT CHAIN 21 153 Interleukin-2.
CC	FT CARBOHYD 23 23 O-Linked (GalNAc . .) (By similarity).
CC	FT CARBOHYD 111 111 N-Linked (GlcNAc . .) (Potential).
CC	FT DISOFID 78 125 By similarity.
CC	FT SEQUENCE 153 AA; 17256 MW; 8173536B2DD0B86 CRC64;
CC	Query Match 70.4%; Score 107; DB 1; Length 153;
CC	Best Local Similarity 70.0%; Pred. No. 8.6e-08;
CC	Matches 21; Conservative 6; Mismatches 3; Indels 0; Ga
Qy 2 APTSSSTKTKTQLOQLEHLLDQMLINGINN 31	
Db 21 APTSSSTKETQEQDQLLDQVLLKGVDN 50	
RESULT 29	SEQUENCE FROM N.A.
Q9MZR9	PRELIMINARY; PRT; 133 AA.
Q9MZR9	AC (TREMBLrel. 15, Created)
Q9MZR9	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
Q9MZR9	DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
Q9MZR9	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
Q9MZR9	DE Interleukin 2 variant IL2delta2.
Q9MZR9	GN Name=IL-2;
Q9MZR9	OS Oryctolagus cuniculus (Rabbit).
Q9MZR9	OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Q9MZR9	OS Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae;
Q9MZR9	NCBI_TaxID=9886;
Q9MZR9	[1]
RN	RP SEQUENCE FROM N.A.
RN	TISSUE=Spine, A.
RX	MEDLINE=201034414; PubMed=10843729; DOI=10.1006/cyto.1999.0658;
RX	Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RX	"The complete cDNA sequences of IL-2, IL-4, IL-6 AND IL-10 from the European rabbit (Oryctolagus cuniculus).",
RX	Cytokine 12:555-565 (2000).
RX	EMBL; AF169168; AAF86652.1; -.
RX	HSSP; P60568; 1IRL.
RX	GO:0005516; C: extracellular; IEA.
RX	GO:0005134; F: interleukin-2 receptor binding; IEA.
RX	GO:00006955; P: immune response; IEA.
RX	InterPro; IPR09019; 4_helix_cycokine.
RX	InterPro; IPR00779; Interleukin-2.
RX	Pfam; PF00715; IL2; 1.
RX	ProDom; P003649; Interleukin-2; 1.
RX	SMART; SM00189; IL2; 1.
RX	PROSITE; PS00424; INTERLEUKIN2; 1.
RX	PS00424; INTERLEUKIN2; 1.
SQ	SEQUENCE 133 AA; 14748 MW; 0D54758C190B5655 CRC64;

Query	2	APTSSTKTKTQLEHILLDQMLINGIN 30	Score 106; DB 2; Length 133;
Best Local Similarity	72.4%	Pred. No. 1e-07;	
Matches	21;	Conservative	5; Mismatches
Matches	21;	Indels	0;
Gaps	0;		
Db	21	APTSSTKTKTQLEHILLDQMLINGIN 49	
RESULT 30			
Q923FT2		PRELIMINARY;	PRT; 155 AA.
ID Q923FT2			
AC AC			
DT 01-DEC-2001	(TREMBLrel.	19, Created)	
DT 01-DEC-2001	(TREMBLrel.	19, Last sequence update)	
DT 01-MAR-2004	(TREMBLrel.	26, Last annotation update)	
DS Interleukin 2.			
OS Sigmodon hispidus (Hispid cotton rat).			
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;			
OC Sigmodon.			
OX NCBI_TaxID=42415;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Darnell M.R.; Pletnev L.M.; Langley R.J.; Blanco J.C.; Prince G.A.;			
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR AF398549; AAK94012; 1;			
HSSP: P60568; 1URL.			
DR GO: GO:0005576; C:extracellular; IEA.			
DR GO; GO:0005134; P:interleukin-2 receptor binding; IEA.			
DR GO; GO:0006595; P:immune response; IEA.			
DR PFAM; PF0715; IL2; 1.			
DR PRINTS; PRO003645; INTERLEUKIN2.			
DR PRODOM; PD003649; Interleukin-2; 1.			
DR SMART; SM0019; IL2; 1.			
DR PROSITE; PS00424; INTERLEUKIN-2; 1.			
SQ SEQUENCE 155 AA; 17627 MW; AC=BA865EB993291 CRC64;			
Query Match	69.7%	Score 106; DB 2; Length 155;	
Best Local Similarity	73.3%	Pred. No. 1.2e-07;	
Matches	22;	Conservative	3; Mismatches
Matches	22;	Indels	5;
Gaps	0;		
Db	21	APTSSTKTKTQLEHILLDQMLINGIN 50	
RESULT 31			
Q923FT2		PRELIMINARY;	PRT; 138 AA.
ID Q923FT2			
AC AC			
DT 01-AUG-1998	(TREMBLrel.	07, Created)	
DT 01-AUG-1998	(TREMBLrel.	07, Last sequence update)	
DT 01-MAR-2004	(TREMBLrel.	26, Last annotation update)	
DS Interleukin-2 (Fragment)			
OS Mesocricetus auratus (Golden hamster).			
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OC Mesocricetus.			
OX NCBI_TaxID=10036;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Spleen;			
RX MEDLINE=98234044; PubMed=9573100;			
RX Melby P.C.; Tryon V.V.; Chandrasekar B.; Freeman G.L.;			
RA "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and			
RT analysis of cytokine mRNA expression in experimental visceral			
RT leishmaniasis.";			
RL Infect. Immun. 66:2135-2142 (1998).			
DR AF046212; 1URL.			
DR HSSP; P0568; 1URL.			
DR GO; GO:0005576; C:extracellular; IEA.			

DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.	FT CHAIN 2 21 155 Interleukin-2.
GO; GO:0006955; P:immune response; IEA.	FT CARBOHYD 23 23 O-linked (GALNAc. . .) (By similarity).
InterPro; IPR00719; 4 helix cytokine.	FT DISULFID 78 126 By similarity.
InterPro; IPR000719; Interleukin-2.	FT SEQUENCE 155 AA; 17632 MW; 67A855A73BF30A CRC64;
Pfam; PF00715; IL2; 1.	Query Match 63.8%; Score 97; DB 2; Length 155;
PRINTS; PRO0285; INTERLEUKIN2.	Best Local Similarity 66.7%; Pred. No. 2; 8e-06;
ProDom; PD003649; Interleukin-2; 1.	Matches 20; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
SMART; SM00189; IL2; 1.	PROSITE; PS000424; INTERLEUKIN_2; 1.
PROSITE; PS000424; INTERLEUKIN_2; 1.	Cytochrome, Glycoprotein, Growth factor; Immune response; Signal;
NON TER 1 1	SIGNAL 1 20 By similarity.
NON TER 138 138 AA; 15739 MW; 35103295670779 CRC64;	CC
SEQUENCE 138 AA; 15739 MW; 35103295670779 CRC64;	CC
Query Match 67.8%; Score 103; DB 2; Length 138;	CC
Best Local Similarity 73.3%; Pred. No. 3e-07; 1.	CC
Matches 22; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	CC
Db 2 APTSSSTKTKTQLEHLILDQMLNGINN 31	CC
Db 14 APTSSKKETQHQLEQQLLDQBLIKGINN 43	CC
RESULT 32	CC
IL2_RAT STANDARD; PRT; 155 AA.	CC
IL2_RAT STANDARD; PRT; 155 AA.	CC
P17108; 01-AUG-1990 (Rel. 15, Created)	CC
DT 01-AUG-1990 (Rel. 15, Last sequence update)	CC
DT 05-JUL-2004 (Rel. 44, Last annotation update)	CC
DT Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).	CC
Name=IL2; Synonyms=IL-2;	CC
Rattus norvegicus (Rat).	CC
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.	CC
NCBI_TaxID=10116; OX	CC
[1] SEQUENCE FROM N.A. MEDLINE=89339608; PubMed=2788130;	CC
McKnight A.J., Mason D.W., Barclay A.M.; "Sequence of rat interleukin 2 and anomalous binding of a mouse interleukin 2 cDNA probe to rat MHC class II-associated invariant chain mRNA."; Immunogenetics 30:145-147 (1989).	CC
-i- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.	CC
-i- SUBCELLULAR LOCATION: Secreted.	CC
-i- SIMILARITY: Belongs to the IL-2 family.	CC
CC	CC
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CC	CC
EMBL; M22899; AAA1427..1; -.	CC
PIR; A43882; A31278..	CC
HSSP; P01585..1M49.	CC
RGD; 620047; IL2..1.	CC
InterPro; IPR009079; 4 helix cytokine.	CC
InterPro; IPR000779; Interleukin-2.	CC
PRINTS; PR00065; INTERLEUKIN2..1.	CC
ProDom; PDD03649; Interleukin-2; 1.	CC
SMART; SM00189; IL2..1.	CC
PROSITE; PS000424; INTERLEUKIN_2..1.	CC
Cytochrome, Glycoprotein, Growth factor; Immune response; Signal;	CC
SIGNAL 1 20 By similarity.	CC
CC	CC
DR X56750; CA440071..1; -.	CC
DR X58428; CA441330..1; -.	CC
DR AB041945; BAB16110..1; -.	CC
DR S16241; S16241..	CC
DR P01585; 1M49..	CC
DR InterPro; IPR009079; 4 helix cytokine.	CC
DR EMBL; X58428; CA441330..1; -.	CC
DR PIR; PR00065; INTERLEUKIN-2..1.	CC
DR PRINTS; PR00065; INTERLEUKIN2..1.	CC
DR ProdDom; PDD03649; INTERLEUKIN-2..1.	CC
DR SMART; SM00189; IL2..1.	CC
DR PROSITE; PDD03649; INTERLEUKIN-2..1.	CC
DR Cytokine; Glycoprotein; Growth factor; Immune response; Signal;	CC
KW	CC

KW	T-cell.	1	20	By similarity.	Best Local Similarity 66.7%; Pred. No. 5.5e-06;
FT	SIGNAL	21	154	Interleukin-2.	Matches 20; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
FT	CHAIN	23	23	O-linked (GAINAC. . .) (By similarity).	
FT	CARBOHYD	78	126	Interleukin-2.	
FT	DISULFID	154	17401 MW;	Interleukin-2.	
SQ	SEQUENCE	154 AA;	F3B95E43D4A3D3E1	CRC64;	
Query Match		63.2%	Score 96; DB 1; Length 15+;	RESULT 35	
Best Local Similarity	66.7%;	Pred. No. 3.9e-06;		Q865X2	PRELIMINARY;
Matches	20;	Conservative	4;	AC	Q865X2
		Mismatches	6;	DR	Q865X2;
		Indels	0;	DR	01-JUN-2003 (TRIMBLrel. 24, Created)
		Gaps	0;	DR	01-JUN-2003 (TRIMBLrel. 24, Last sequence update)
				DR	01-MAR-2004 (TRIMBLrel. 26, Last annotation update)
				DE	Interleukin 2.
				GN	Name=IL-2;
				OS	Lama glama (Llama).
				OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
				OC	Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
				OX	NCBI_TaxID=9844;
				RN	[1]
				RP	SEQUENCE FROM N.A.
				RA	Baadan O., Lee S.-., Yoshida R., Chang K.-., Ohashi K., Sugimoto C., Onuma M.,
				RA	Submitted (APR-2003) to the EMBL/GenBank/DBBJ databases.
				RL	EMBL: AB107651; BAC533881; -.
				DR	HSSP; P60568; 1RL.
				DR	GO; GO:0005576; C:extracellular; IEA.
				DR	GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
				DR	GO; GO:0005955; P:immune response; IEA.
				DR	IntterPro; IPR000779; Interleukin-2.
				DR	PFam; PF00715; IL2; 1.
				DR	PRINTS; PR00265; INTERLEUKIN2.
				DR	ProDom; PD003649; Interleukin-2; 1.
				DR	SMART; SM0019; IL2; 1.
				DR	PROSITE; PS00424; INTERLEUKIN-2; 1.
				SQ	SEQUENCE 154 AA; 17652 MW; 8020RC8DB7BABA38 CRC64;
				Query Match	61.2%; Pred. No. 1.1e-05;
				Best Local Similarity	66.7%; Pred. No. 1.1e-05;
				Matches	20; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
				Q8	RESULT 36
				AC	IL2_HORSE STANDARD;
				AC	P37597;
				DT	01-OCT-1994 (Rel. 30, Created)
				DT	01-NOV-1995 (Rel. 32, Last sequence update)
				DB	Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
				GN	Name=IL2;
				OS	Equus caballus (Horse).
				OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
				OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
				OX	NCBI_TaxID=9796;
				RN	[1]
				RP	SEQUENCE FROM N.A.
				RX	MEDLINE=9160538; PubMed=8116217; DOI=10.1016/0165-2427(93)90070-K;
				RA	Vandergrift E.V., Horovitz D.W.,
				RT	"Molecular cloning and expression of equine interleukin 2."
				RL	Vet. Immunol. Immunopathol. 39:395-406(1993).
				CC	SEQUENCE FROM N.A.
				CC	Tavernor A.S., Allen W.R., Butcher G.W.; Submitted (NOV-1992) to the EMBL/GenBank/DBBJ databases.
				CC	-1- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.
				CC	-1- SIMILARITY: Belongs to the IL-2 family.
				CC	-----
				CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
				CC	-----
				DR	EMBL; X68779; CA48679.1; -.
				DR	InterPro; IPR00979; 4 helix_cytokine.
				DR	PFam; PF00715; IL2; 1.
				DR	PRINTS; PR00265; INTERLEUKIN2.
				DR	ProDom; PD003649; Interleukin-2.
				DR	SMART; SM00189; IL2; 1.
				DR	PROSITE; PS00424; INTERLEUKIN 2; 1.
				DR	Cytokine; Glycoprotein; Growth Factor; Immune response; Signal; T-cell.
				FT	1 20 By similarity.
				FT	CHAIN 21 155 Interleukin-2.
				FT	23 23 O-linked (GAINAC. . .) (By similarity).
				FT	CARBOHYD 78 126 By similarity.
				FT	DISULFID 155 AA; 17602 MW; D0F7AA1A81CDDA CRC64;
				SQ	SEQUENCE 62.5%; Score 95; DB 1; Length 155;
				Query Match	

CC	mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.	Best Local Similarity 90.5%; Pred. No. 2.6e-06; Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0
CC	-1- SUBCELLULAR LOCATION: Secreted.	Qy 4 TSSSTKTKTQLEHLLQMLDQ 24 Db 3 TSXSTKTKTQLEHLLQMLDQ 23
CC	-1- SIMILARITY: Belongs to the IL-2 family.	RESULT 38 IL2_ORCOR ID 097513; DT 30-MAY-2000 (Rel. 39, Created) DT 30-MAY-2000 (Rel. 39, Last sequence update) DT 05-JUL-2004 (Rel. 44, Last annotation update) DB Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGP) (Fragment). DB (Name:IL2; GN Orcinus orca (Killer whale). OS Orcinus orca RA Ness T.L., Bradley W.G., Reynolds J.B., III, Roess W.B.; RT "Isolation and expression of the interleukin-2 gene from the killer whale, Orcinus orca."; RL Mar. Mamm. Sci. 14:531-543 (1998). RN SEQUENCE FROM N.A. RP RA Ness T.L., Bradley W.G., Reynolds J.B., III, Roess W.B.; RT "Isolation and expression of the interleukin-2 gene from the killer whale, Orcinus orca."; RL Mar. Mamm. Sci. 14:531-543 (1998). -1- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells (By similarity). -1- SUBCELLULAR LOCATION: Secreted. -1- SIMILARITY: Belongs to the IL-2 family. CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - PROSITE: PS00424; INTERLEUKIN 2; 1. Cytokine; Glycoprotein; Growth factor; Immune response; Signal; T-cell. PRINTS: PR00265; INTERLEUKIN2. PRODOM: PD00369; Interleukin-2; 1. SMART: SM00189; IL2; 1. PROSITE: PS00424; INTERLEUKIN 2; 1. Cytokine; Glycoprotein; Growth factor; Immune response; Signal; T-cell. SIGNAL 1 20 By similarity. CHAIN 21 149 Interleukin-2. FT By similarity. DISULFID 78 121 O-linked (GalNAc. . .) (By similarity). CARBOHYD 23 23 N-linked (GlcNAc. . .) (Potential). CARBOHYD 106 106 3 R -> K (in Ref. 2). CONFLICT 3 3 S -> A (in Ref. 2). CONFLICT 8 8 S -> A (in Ref. 2). CONFLICT 59 59 I -> M (in Ref. 2). CONFLICT 125 125 N -> D (in Ref. 2). CONFLICT 128 128 E -> G (in Ref. 2). CONFLICT 145 145 I -> F (in Ref. 2). CONFLICT 148 148 L -> M (in Ref. 2). SEQUENCE 149 AA; 17086 MW; 051BB8C47A0114FC CRC64; Query Match 2 APTSSSTKTKTQLEHLLQMLDQ 31 Best Local Similarity 60.5%; Pred. No. 1.5e-05; Matches 17; Conservative 8; Mismatches 5; Indels 0; Gaps 0; Db 21 APTSSSTKTKTQLEHLLQMLDQLEGVN 50
CC	CC	RESULT 37 Q9UCP5 ID Q9UCP5; PRELIMINARY; PRT; 23 AA. AC 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update) DB Interleukin 2 (Fragment). Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606; SEQUENCE [1] RN RP RX MEDLINE:93289963; PubMed:8512072; DOI=10.1006/abio.1993.1209; Mulinier S., Karzenev B., Triplier D.; "Charge heterogeneity of insulin fusion proteins expressed in Escherichia coli is not due to proteolytic degradation."; Anal. Biochem. 210(1):366-373 (1993). SEQUENCE 23 AA; 2637 MW; 40B64C6875EB021F CRC64;
CC	CC	Query Match 57.9%; Score 88; DB 1; Length 152; Best Local Similarity 60.0%; Pred. No. 6e-05; Matches 18; Conservative 6; Mismatches 6; Indels 0; Gaps 0 Db 2 APTSSSTKTKTQLEHLLQMLDQ 31 21 APTSSSTKTKTQLEHLLQMLDQ 50

RESULT 39	Q7IV48	PRELIMINARY;	PRT;	38 AA.	Qy	2 APSSSTKTKTQLEHILLDLOMLINGINN 31
ID	Q7IV48				Db	21 APSSSTENTKQQVSLQDHLRINN 50
AC	Q7IV48;					
DR	05-JUL-2004	(TREMBLrel. 27, Created)				
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)				
DR	05-JUL-2004	(TREMBLrel. 27, Last annotation update)				
DE	Interleukin-2 (Fragment).					
OS	Homo sapiens (Human).					
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;					
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
NCBI_TAXID=9606;						
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Turner D.M., Simnot P.J., Hutchinson I.V.;					
RL	Submitted (Oct-1997) to the EMBL/Genbank/DBJ databases.					
DR	EMBL; AF031845; BAB86661.1;					
DR	GO; GO:0005576; C:extracellular; IEA.					
DR	GO; GO:005134; F:interleukin-2 receptor binding; IEA.					
DR	GO; GO:0006955; F:immune response; IEA.					
DR	InterPro; IPR000779; Interleukin-2.					
DR	PF00715; IL2; 1.					
DR	ProDom; PD003649; Interleukin-2; 1.					
FT	NON_TER 38					
SEQUENCE	38 AA; 4192 MW; 8D84AE5144C2CBA3 CRC64;					
Qy	2 APSSSTKTKTQLEHILL 19					
Db	21 APSSSTKTKTQLEHILL 38					
Query Match	57.2%	Score 87;	DB 2;	Length 38;		
Best Local Similarity	100.0%	Pred. No. 1.8e-05;				
Matches	18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	2 APSSSTKTKTQLEHILL 19					
Db	21 APSSSTKTKTQLEHILL 38					
RESULT 40	Q9XT84	PRELIMINARY;	PRT;	154 AA.		
ID	Q9XT84					
AC	Q9XT84;					
DR	01-NOV-1999 (TREMBLrel. 12, Created)					
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)					
DR	01-MAR-2004 (TREMBLrel. 26, Last annotation update)					
DE	Interleukin 2.					
OS	Delphinapterus leucas (Beluga whale).					
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;					
OC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;					
OC	Monodontidae; Delphinapterus.					
NCBI_TAXID=9749;						
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=99221046; PubMed=10206205; DOI=10.1016/S0165-2427(99)00009-4;					
RA	St-Laurent G., Beliveau C., Archambault D.;					
RT	"Molecular cloning and phylogenetic analysis of beluga whale (Delphinapterus leucas) and gray seal (Halichoerus grypus) interleukin 2."					
RT	Vet. Immunol. Immunopathol. 67:385-394(1999).					
DR	EMBL; AF072870; ADD4047.1;					
DR	HSSP; B60568; IL2L.					
DR	GO; GO:0005576; C:extracellular; IEA.					
DR	GO; GO:005134; F:interleukin-2 receptor binding; IEA.					
DR	GO; GO:0006955; F:immune response; IEA.					
DR	InterPro; IPR003079; 4-heelix-cytokine.					
DR	InterPro; IPR000779; Interleukin-2.					
DR	PF00715; IL2; 1.					
DR	PRINTS; PRO0265; INTERLEUKIN2.					
DR	ProDom; PD003649; Interleukin-2; 1.					
DR	SMART; SM00189; IL2; 1.					
DR	PROSITE; PS00424; INTERLEUKIN-2; 1.					
SEQUENCE	154 AA; 17652 MW; 4288D3D41D04F172 CRC64;					
Qy	54.6%	Score 83;	DB 2;	Length 154;		
Best Local Similarity	56.7%	Pred. No. 0.00034;				
Matches	17;	Conservative 6;	Mismatches 7;	Indels 0;	Gaps 0;	

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OM protein - protein search, using sw model

Run on: September 23, 2005, 12:40:19 ; Search time 24,3934 Seconds
(without alignments)
122,275 Million cell updates/sec

Title: US-10-727-514-2

Perfect score: 152
Sequence: MAPTSSSTKTKTQLQLEHLLLDLQMLINGINN 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0\$

Maximum Match 100\$

Listing First 100 summaries

Database : PIR_79;*

1: PIR1;*

2: PIR2;*

3: PIR3;*

4: PIR4;*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query Match	Length	DB ID	Description
1	147	96.7	153	1 ICG12	interleukin-2 prec
2	147	96.7	153	1 ICHU2	interleukin-2 prec
3	114	75.0	154	2 JN0998	interleukin 2 prec
4	97	63.8	155	2 A31278	interleukin-2 prec
5	96	63.2	154	2 S16241	interleukin-2 prec
6	95	62.5	155	2 S3359	interleukin-2 - Mo
7	92	60.5	149	2 S3191	interleukin-2 prec
8	79	52.0	155	2 I45913	interleukin-2 prec
9	79	52.0	155	2 S38662	interleukin-2 - go
10	79	52.0	155	2 S11488	interleukin-2 prec
11	69	45.4	169	2 S37289	interleukin-2 prec
12	64	42.1	169	1 ICMS2	interleukin-2 prec
13	59.5	39.1	60	2 I68870	interleukin 2 - we
14	57.5	38.5	62	2 I54512	interleukin 2 - mo
15	57.5	37.8	62	2 I68871	interleukin 2 - mo
16	54	35.5	357	2 S12169	isopenicillin N ac
17	52	34.2	155	1 F64145	hypothetical prote
18	52	34.2	737	2 G82262	probable exopolya
19	51	33.6	304	2 F95285	probable Ly4R-type
20	51	33.6	627	2 E70122	flagellar hook-ass
21	50	32.9	365	2 C70701	hypothetical prote
22	49	32.2	230	2 H82247	DNA-binding respon
23	49	32.2	543	2 F82217	methyl-accepting C
24	49	32.2	1130	2 A89130	protein F5E1.4 [i]
25	48.5	31.9	240	2 T22210	hypothetical prote
26	48	31.6	189	2 H64107	hypothetical prote
27	48	31.6	441	2 A81367	aminopeptidase C
28	48	31.6	441	2 AC136	G protein-coupled
29	48	31.6	595	2 JC8012	

ALIGNMENTS

RESULT 1

ICG12
interleukin-2 precursor - common gibbon
N;Alternate names: IL-2; T-cell growth factor
C;Species: Hylobates lar (common gibbon, white-handed gibbon)
C;Accession: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
R;Chen, S.J.; Holbrook, N.J.; Mitchell, K.F.; Vallone, C.A.; Crabtree, Proc. Natl. Acad. Sci. U.S.A. 82, 7284-7288, 1985
A;Title: A viral long terminal repeat in the interleukin 2 gene of a cell line that cons
A;Reference number: A94067; MUID:3877307
A;Accession: A94067
A;Molecule type: mRNA
A;Residues: 1-153 <CHE>
A;Cross-references: UNIPROT:P60569; GB:MI1144; NID:9177014; PIDN:AAA35454.1; PID:9177015
A;Experimental source: leukemia cell line MLA 144; ATCC TIB 201
C;Superfamily: interleukin-2
C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell
P;1-20 Domain: signal sequence #status predicted <SIG>
P;21-153/Product: interleukin-2 #status predicted <IL2>
P;23/Binding Site: carbonylate (Thr) (covalent) #status predicted
P;78-125/Disulfide bonds: #status predicted

Query Match 96.7% Score 147; DB 1; Length 153;
Best Local Similarity 100.0% Pred. No. 3.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 APSSSTRKTQLEHLLDQMLNGINN 31
Db 21 APSSSTRKTQLEHLLDQMLNGINN 50

RESULT 2
ICUH2
interleukin-2 precursor [validated] - human
N;Alternate names: IL-2; T-cell growth factor
C;Species: Homo sapiens (man)
C;Date: 11-Aug-1983 #sequence revision 11-Aug-1983 #text_change 09-Jul-2004
C;Accession: A01849; P21192; A2961; S3109; A93297; A90113; A93478; I56518; I52
R;Holbrook, N.J.; Lieber, M.; Crabtree, G.R.
Nucleic Acids Res. 12, 5005-5013, 1984
A;Title: DNA sequence of the 5' flanking region of the human interleukin 2 gene: homolog
A;Reference number: A93524; MUID:84247353; PMID:6330695
A;Accession: A01849
A;Molecule type: DNA
A;Residues: 1-153 <HOL>
A;Cross-references: UNIPROT:P60568; GB:MI00695; GB:X00200; GB:X00201; GB:X00202; NID:9337
R;Fujita, T.; Takaoka, C.; Matsui, H.; Taniguchi, T.
Proc. Natl. Acad. Sci. U.S.A. 80, 7437-7441, 1983
A;Title: Structure of the human interleukin 2 gene.
A;Reference number: A21192; MUID:84170243; PMID:6324170
A;Molecule type: DNA
A;Residues: 1-153 <FNU>
A;Cross-references: GB:J00264; PIDN:AAA86284; PID:9186284; PIDN:AAA8509.1; PID:9186286
R;Holbrook, N.J.; Smith, K.A.; Fornace Jr., A.J.; Comeau, C.M.; Wiskocil, R.L.; Crabtree Proc. Natl. Acad. Sci. U.S.A. 81, 1634-1638, 1984
A;Title: T-cell growth factor: complete nucleotide sequence and organization of the gene
A;Reference number: A20961; MUID:84170356; PMID:6608729
A;Accession: A20961
A;Molecule type: DNA
A;Residues: 1-153 <HO2>
A;Cross-references: GB:K02056; NID:9186302; PIDN:AAA98792.1; PID:9386819
R;Laabs, Y.; Gras, M.F.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, ENBO J. 11, 3897-3904, 1992
A;Title: A new gene, FCM, on chromosome 16 is fused to the interleukin 2 gene by a t (4;1
A;Reference number: S31208; MUID:93010984; PMID:1395683
A;Accession: S31209
A;Molecule type: mRNA

A;Residues: 11-117 <LAA>
A;Cross-references: EMBL:Z14955
A;Note: this sequence is shown from the beginning of the fragment to the chromosomal break
R;Taniguchi, T.; Matsui, H.; Fujita, T.; Takaoka, C.; Kashima, N.; Yoshimoto, R.; Hamuro Nature 302, 305-310, 1983
A;Title: Structure and expression of a cloned cDNA for human interleukin-2.
A;Reference number: A93297; MUID:83167472; PMID:6403867
A;Accession: A93297
A;Molecule type: mRNA
A;Residues: 1-153 <TAN>
A;Cross-references: GB:V00564; NID:933780; PIDN:CAA23827.1; PID:95729676
A;Experimental source: leukemic T-cell line, Jurkat-111, cloned from Jurkat-FHCR
R;Maeda, S.; Nishino, N.; Obaru, K.; Mita, S.; Noniwaya, H.; Shimada, K.; Fujimoto, K.; Biochem. Biophys. Res. Commun. 115, 1040-1047, 1983
A;Title: Cloning of interleukin 2 mRNAs from human tonsils.
A;Reference number: A90113; MUID:84023840; PMID:6312994
A;Accession: A90113
A;Molecule type: mRNA
A;Residues: 1-153 <MAB>
A;Cross-references: GB:J00264; NID:9186294; PIDN:AAA23827.1; PID:95729676
A;Experimental source: tonsilar mononuclear cells
R;Devoe, R.; Plaetinck, G.; Cheron, H.; Degraeve, W.; Tavernier, J.; Remaury, N.; Simons, G.; Schwartz, M.
Nucleic Acids Res. 11, 4307-4323, 1983
A;Title: Molecular cloning of human interleukin 2 cDNA and its expression in Escherichia coli
A;Reference number: A93478; MUID:83246551; PMID:6306584
A;Accession: A93478
A;Molecule type: mRNA
A;Residues: 1-153 <DEV>
A;Cross-references: GB:V00564; NID:933780; PIDN:CAA23827.1; PID:933781
A;Experimental source: epilenoocytes
R;Bizenberg, O.; Faber-Elman, A.; Lotan, M.; Schwartz, M.
J. Neurochem. 64, 1328-1336, 1995
A;Title: Interleukin-2 mRNAs in human and rodent brains: possible expression by astrocytes
A;Reference number: I56518; MUID:95239150; PMID:7722480
A;Accession: I56518
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-152 <ELZ>
A;Cross-references: GB:S77834; NID:9999000
A;Accession: I73624
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 5-/, P-9-17, 'P'-19-32, 'X'-34-45, 'X'-47-143 <REBS>
A;Cross-references: GB:S77835; NID:9999001; PIDN:AA11264.1; PID:94261964
R;Nishino, N.; Obaru, K.; Maeda, S.; Shimada, K.; Onoue, K.
Biomed. Res. 6, 197-205, 1985
A;Title: Organization of the DNA regions flanking the human interleukin 2 gene.
A;Reference number: I57603; MUID:87064618; PMID:1491296
A;Accession: I52528
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-68 <RE2>
A;Cross-references: GB:M33199; NID:9186296; PIDN:AA59139.1; PID:9553508
R;Siebenlist, U.; Durand, D.B.; Bressler, P.; Holbrook, N.J.; Norris, C.A.; Kamoun, M.; Mol. Cell. Biol. 6, 3042-3049, 1986
A;Title: Promoter region of interleukin-2 gene undergoes chromatin structure changes and A;Reference number: I57603; MUID:87064618; PMID:1491296
A;Accession: I57603
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-68 <RE3>
A;Cross-references: GB:M13879; NID:9186305; PIDN:AA59141.1; PID:9553509
R;Weir, M.P.; Chaplin, M.A.; Wallace, D.M.; Dykes, C.W.; Hobden, A.N.
Biochemistry 27, 6883-6892, 1988
A;Title: Structure-activity relationships of recombinant human interleukin 2.
A;Reference number: I52401; MUID:8906220; PMID:1264184
A;Contents: recombinant IL-2 and mutants expressed in E. coli
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 'W'-21-153 <RE4>
A;Cross-references: GB:M22005; NID:9186300; PIDN:AA59140.1; PID:9386818
A;Note: mutation of Phe-42 to Ala reduced binding to the IL-2 receptor 5-10 fold without

R;Robb, R.J.; Kurnty, R.M.; Panico, M.; Morris, H.R.; Chowdhry, V.
Proc. Natl. Acad. Sci. U.S.A. 81: 6486-6490, 1984
A;Title: Amino acid sequence and post-translational modification of human interleukin 2.
A;Reference number: A94009; MUID:85038540; PMID:6333684

A;Molecule type: protein

A;Residues: 21-153 <R>C>

A;Note: disulfide bonds and carbohydrate binding site were determined in Jurkat-derived IL-2 is primarily due to differences in glycosylation 21-Ala (Fr-IL2-A and Fr-IL2-B) and 22-Pro (Fr-IL2-B)
R;Conradt, B.; Hofer, B.; Nimtz, M.; Jaeger, V.; Conradt, H.S.
Bur. J. Biochem. 215, 189-197, 1993

A;Title: Biosynthesis and secretion of human interleukin 2 glycoproteins variants from 26, 17368-17373, 1989
A;Contents: annotation; glycosylation of variant forms expressed in insect cells

C;Genetics:

A;Gene: GDB:IL2

A;Cross-references: GDB:147680

A;Map position: 4q26.4q27

A;Introns: 49/3; 69/3; 117/3

C;Superfamily: interleukin-2

C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell

F;A20/Domain: signal sequence #status predicted <S>G>

F;21-153/Product: interleukin-2 #status experimental <IL2>

F;23/Banding site: carbohydrate (Thr) (covalent) #status experimental
F;78-125/Diulfide bonds: #status experimental

A;Best Local Similarity 96.7%; Score 147; DB 1; Length 153;

A;Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

A;Reference number: A94463; MUID:90008901; PMID:2793860
A;Accession: A34463
A;Molecule type: protein
A;Residues: 21-35 <CON>

A;Note: the O-linked glycosylation site in recombinant material matched that from human

R;Grabenhorst, E.; Hofer, B.; Nimtz, M.; Jaeger, V.; Conradt, H.S.

Bur. J. Biochem. 215, 189-197, 1993

A;Title: Biosynthesis and secretion of human interleukin 2 glycoproteins variants from 26, 17368-17373, 1989
A;Contents: annotation; glycosylation of variant forms expressed in insect cells

C;Genetics:

A;Gene: GDB:IL2

A;Cross-references: GDB:147680

A;Map position: 4q26.4q27

A;Introns: 49/3; 69/3; 117/3

C;Superfamily: interleukin-2

C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell

F;A20/Domain: signal sequence #status predicted <S>G>

F;21-153/Product: interleukin-2 #status experimental <IL2>

F;23/Banding site: carbohydrate (Thr) (covalent) #status experimental
F;78-125/Diulfide bonds: #status experimental

A;Best Local Similarity 96.7%; Score 147; DB 1; Length 153;

A;Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-154 <CO2>

A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:9304313; PIDN:AAA02865.1; PMID:9304314

C;Superfamily: interleukin-2

C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;

A;Best Local Similarity 73.3%; Score 5; DB 2; Length 154;

A;Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

A; Reference number: S33509	Qy	2 APTSSSTKTKTQLQLEHLLDQLMINGINN 31
A; Status: preliminary	Db	21 APTSSSTGNTMKEVSKLQLDQLLEKVN 50
A; Molecule type: mRNA		
A; Residues: 1-155 <PRL>		
A; Cross-references: UNIPROT:Q08081; EMBL:X68779; PIDN:9577588; PIDN:CAR48679.1; PID:93116		
C; Superfamily: interleukin-2		
RESULT 9		
S38662		
Interleukin-2 - Goat		
C;Species: Capra aegagrus hircus (domestic goat)		
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004		
R;Rimata, E.		
submitted to the EMBL Data Library, November 1993		
A;Description: The molecular cloning and expression of caprine interleukin 2.		
A;Reference number: S38662		
A;Accession: S38662		
A;Status: preliminary		
A;Molecule type: mRNA		
A;Cross-references: UNIPROT:P36835; EMBL:X76063; PIDN:9416002; PIDN:CAA53664.1; PID:94160		
C;Superfamily: interleukin-2		
RESULT 7		
S31391		
interleukin-2 precursor - horse		
C;Species: Equus caballus (domestic horse)		
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004		
R;Taverner, A.S.; Butcher, G.W.		
submitted to the EMBL Data Library, November 1992		
A;Description: cDNA cloning of equine interleukin-2 by polymerase chain reaction.		
A;Accession: S31391		
A;Status: preliminary		
A;Molecule type: mRNA		
A;Residues: 1-149 <PRL>		
A;Cross-references: UNIPROT:P37997; EMBL:X69393; PIDN:91076; PIDN:CAA49190.1; PID:91077		
C;Superfamily: interleukin-2		
RESULT 10		
S11488		
interleukin-2 precursor - sheep		
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)		
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004		
R;Seow, H.F.; Rothel, J.S.; Padford, A.J.; Wood, P.R.		
C;Accession: S11488; S13102; S15517		
R;Goodall, J.C.; Emery, D.C.P.; Perry, A.C.P.; English, L.S.; Hall, L.		
Nucleic Acids Res. 18, 5883, 1990		
A;Title: The molecular cloning of ovine interleukin 2 gene by the polymerase chain react		
A;Reference number: S13102; PMID:91088336; PMID:2263496		
A;Accession: S11488		
A;Status: preliminary		
A;Molecule type: mRNA		
A;Residues: 1-155 <PRL>		
A;Cross-references: UNIPROT:P19114; EMBL:X53934; PIDN:CAA39165.1; PID:91811		
R;Bridges, R.; Williamson, M.L.; Sargan, D.R.; Hein, W.H.; McConnell, I.		
Submitted to the EMBL Data Library, April 1991		
A;Accession: S115517		
A;Status: preliminary		
A;Molecule type: mRNA		
A;Residues: 1-5 ,L ,7-155 <PRL>		
A;Cross-references: EMBL:X5541; PIDN:91810; PIDN:CAA39165.1; PID:91811		
R;Anikeeva, N.N.; Vinogradova, T.V.; Vosobhin, O.N.		
Submitted to the EMBL Data Library, December 1989		
A;Reference number: S21470		
A;Accession: S21470		
A;Molecule type: DNA		
A;Residues: 1-22 <AN2>		
A;Cross-references: EMBL:X17201; PIDN:9452; PIDN:CAA35062.1; PID:9453		
C;Genetics:		
A;Gene: IL-2		
C;Superfamily: interleukin-2		
C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell		
Query Match 52.0%; Score 79; DB 2; Length 155;		
Best Local Similarity 53.3%; Pred. No. 0.00034;		
Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;		
Qy 2 APTSSSTKTKTQLQLEHLLDQLMINGINN 31		
Db 21 APTSSSTGNTMKEVSKLQLDQLLEKVN 50		

RESULT 11
 S37289 interleukin-2 precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 A;Cross-references: S37289; S27205; S36162; S2936
 A;Accession: S37289
 A;Reference number: S37289
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-169 <RKS>
 A;Cross-references: EMBL:X73040
 A;Cross-references: UNIPROT:Q8BHA4; EMBL:X73040
 A;Title: A new cDNA sequence for the murine interleukin-2 gene.
 A;Reference number: S27205; PMID:93041941; PMID:1420317
 A;Accession: S27205
 A;Molecule type: mRNA
 A;Residues: 1-63 <NAME>
 A;Cross-references: EMBL:X66058; PIDN:CAA46854_1; PID:952726
 R;Ghosh, S.; Palmer, S.M.; Rodrigues, N.R.; Cordell, H.J.; Hearne, C.M.; Cornall, R.J.;
 A;Title: Polycyclic control of autoimmune diabetes in nonobese diabetic mice.
 A;Reference number: S36162; PMID:9404970; PMID:8401590
 A;Status: preliminary
 A;Residues: 1-50 <GHO>
 A;Cross-references: EMBL:X73040
 C;Superfamily: interleukin-2
 C;Keywords: cytokine; glycoprotein; growth factor; lymphokine; T-cell
 C;Sequence: 1-20
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-63/Domain: interleukin-2 #status predicted <MAT>
 Query Match 45.4% Score 69; DB 2; Length 169;
 Best Local Similarity 47.2%; Pred. No. 0.011; 6; Mismatches 7; Indels 6; Gaps 1;
 Matches 17; 'Conservative' 6;
 Qy 2 APTSSSTKTKTQ-----LHLHLQMLNGINN 31
 Db 29 SPTSSSTAAQQQQQQHQEQLMDLQELLSRMEN 64
 A;Accession: A93550
 A;Molecule type: DNA
 A;Residues: 1-169 <RKS>
 A;Cross-references: UNIPROT:P04351
 R;Degraeve, W.; Simons, G.; Davos, R.; Plaetinck, G.; Remaut, E.; Tavernier, J.; Fiers, W.
 A;Title: Cloning and structure of a mouse interleukin-2 chromosomal gene.
 A;Reference number: A54490; PMID:86118396; PMID:3003564
 A;Accession: A54490
 A;Molecule type: DNA
 A;Residues: 1-169 <PUS>
 A;Cross-references: UNIPROT:MI6760
 A;Cross-references: GB:MI6760
 A;Title: Use of a cDNA expression vector for isolation of mouse interleukin-2 cDNA clone
 A;Reference number: 148597; PMID:8511148; PMID:2578624
 A;Accession: 148597
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-169 <RKS>
 A;Cross-references: EMBL:X01772; GB:K02797; PIDN:CAA25909_1; PMID:9758159
 C;Comment: Produced by T-cells in response to antigenic or mitogenic stimulation, this is
 C;Genetics:
 A;Introns: 63/3; 83/3; 132/3
 C;Superfamily: interleukin-2
 C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-169/Domain: interleukin-2 #status predicted <MAT>
 F;23/Binding site: carbohydrate (tar) (covalent) #status predicted
 F;92-140/Disulfide bonds: #status predicted
 Query Match 42.1% Score 64; DB 1; Length 169;
 Best Local Similarity 38.6%; Pred. No. 0.061; 6; Mismatches 7; Indels 14; Gaps 1;
 Matches 17; 'Conservative' 6;
 Qy 2 APTSSST-----KKTQOLEHLQMLNGINN 31
 Db 21 APTSSSTSSSTAEEQQQQQQHQEQLMDLQELLSRMEN 64
 RESULT 13
 I68870 interleukin 2 - western wild mouse (fragment)
 C;Species: Mus spretus (western wild mouse)
 C;Date: 02-Aug-1995 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 R;Matesanz, F.; Alcina, A.; Pellicer, A.
 Immunogenetics 38, 300-303, 1993
 A;Title: Existence of at least five interleukin-2 molecules in different mouse strains.
 A;Reference number: 154512; PMID:9330771; PMID:8319981
 A;Accession: 168870
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-60 <RKS>
 A;Cross-references: UNIPROT:Q08867; GB:L07575; PID:934951; PMID:9339327_1; PID:934951
 C;Genetics:
 A;Gene: IL-2
 C;Superfamily: interleukin-2
 Query Match 39.1% Score 59.5; DB 2; Length 60;
 Best Local Similarity 45.5%; Pred. No. 0.088; 6; Mismatches 5; Indels 7; Gaps 1;
 Matches 15; 'Conservative' 6;
 Qy 2 APTSSST-----KKTQOLEHLQMLNGINN 27
 Db 25 SPTSSSTSSSTAEEQQQQHQEQLMDLQELLSRMEN 57
 RESULT 14
 I54512 interleukin 2 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Aug-1995 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
 R;Matesanz, F.; Alcina, A.; Pellicer, A.
 Immunogenetics 38, 300-303, 1993
 A;Title: Existence of at least five interleukin-2 molecules in different mouse strains.
 A;Reference number: 154512; PMID:9330771; PMID:8319981
 A;Accession: 154512
 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
 A;Residues: 1-62 <RES>
 A;Cross-references: GB:LO7574; NID:9349513; PIDN:AAA39326.1; PMID:9349514
 C;Genetics:
 A;Gene: IL-2
 C;Superfamily: interleukin-2
 C;Superfamily: interleukin-2

Query Match 38.5%; Score 58.5; DB 2; Length 62;
 Best Local Similarity 42.9%; Pred. No. 0.13;
 Matches 15; Conservative 6; Mismatches 5; Indels 9; Gaps 1;

Qy 2 APTSSST-----KTKTQLEHLLIDLQMLN 27
 Db 25 SPTSSSTSSATAQQQQQHQEQLLMDLQELS 59

RESULT 15
 I68871
 Interleukin 2 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: 168871
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
 R;Matesanz, F.; Alcina, A.
 R;Immunogenetics 38, 300-303, 1993
 A;Title: Existence of at least five interleukin-2 molecules in different mouse strains.
 A;Reference number: 154512; PMID:93307791; PMID:8319981
 A;Accession: 168871
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-72 <RES>
 A;Cross-references: GB:LO7576; NID:9349517; PIDN:AAA39328.1; PMID:9349518
 C;Genetics:
 A;Gene: IL-2
 C;Superfamily: interleukin-2

Query Match 37.8%; Score 57.5; DB 2; Length 72;
 Best Local Similarity 35.6%; Pred. No. 0.21;
 Matches 16; Conservative 5; Mismatches 5; Indels 19; Gaps 1;

Qy 2 APTSSSTKTKTOL-----LEHLLIDLQMLN 27
 Db 25 SPTSSSTSSATAQQQQQQQQQQQQQQQQQQQQQHLEQLLMDLQELS 69

RESULT 16
 S12169
 Isopenicillin N acyltransferase (EC 2.3.1.1) - *Emericella nidulans*
 N;Alternative names: acyl coenzyme A-6-aminopenicillanic acid acyltransferase; acyltransferase
 C;Species: *Emericella nidulans*, *Aspergillus nidulans*
 C;Accession: S12169, A36142; S09090
 R;Montenegro, E.; Barredo, J.L.; Gutierrez, S.; Diez, B.; Alvarez, E.; Martin, J.F.
 Mol. Gen. Genet. 221, 322-330, 1990
 A;Title: Cloning, characterization of the acyl-CoA:6-amino penicillanic acid acyltransferase
 A;Reference number: S12169; PMID:90340281; PMID:2166227
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-357 <MON>
 A;Cross-references: UNIPROT: P21133; EMBL:X53310; NID:g2378; PIDN:CAA37394.1; PMID:g2379
 R;Tobin, M.B.; Fleming, P.L.; Miller, J.R.
 J;Bacteriol. 172, 5908-5914, 1990
 A;Title: Molecular characterization of the acyl-coenzyme A:isopenicillin N acyltransferase
 A;Reference number: A36142; PMID:91008967; PMID:2120195
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-357 <TOB>
 A;Cross-references: GB:MS6293; NID:g167999; PIDN:AAA33287.1; PMID:g168000
 R;Whiteman, E.P.; Baldwin, J.E.; Fleming, M.D.; Schofield, C.J.; Sutherland
 FEBS Lett. 262, 342-344, 1990
 A;Title: Acetyl coenzyme A: 6-aminopenicillanic acid acyltransferase from *Penicillium chrysogenum*

A;Reference number: S09089; MUID:90242961; PMID:2110531
 A;Accession: S09090
 A;Molecule type: protein
 A;Residues: 103-122 <WHI>
 C;Genetics:
 A;Introns: 12/3; 71/1; 121/3
 C;Keywords: acyltransferase

Query Match 35.5%; Score 54; DB 2; Length 357;
 Best Local Similarity 52.6%; Pred. No. 4.1;
 Matches 10; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 8 TKTKTQLEHLLIDLQMLN 26
 Db 40 TKTKTQALEQQLIREEQVM 58

RESULT 17
 F64145
 hypothetical protein HI0227 - *Haemophilus influenzae* (strain Rd KW20)
 C;Species: *Haemophilus influenzae*
 C;Accession: F64145
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 R;Pleischnmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Kerlavage, R.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, C.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 265, 456-511, 1995
 A;Authors: Gneim, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
 A;Reference number: A64000; MUID:9535060; PMID:7542800
 A;Accession: F64145
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-155 <TIGR>
 A;Cross-references: UNIPROT:P44583; GB:U32709; PIDN:91573190; PIDN: AAC21897.1;
 C;Superfamily: hypothetical protein HI0227

Query Match 34.2%; Score 52; DB 1; Length 155;
 Best Local Similarity 29.0%; Pred. No. 3.2;
 Matches 9; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MAPTSSSTKKNQQLQHLLIDLQMLN 31
 Db 50 NEPETRPSSKKRKAELHKEYLDQVLRGTE 80

RESULT 18
 GB2262
 probable exopolysaccharide biosynthesis protein VC0937 [imported] - *Vibrio cholerae* (str. C;Species: *Vibrio cholerae*
 C;Accession: GB2262
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 R;Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Richardson, D.; Brzozowska, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
 A;Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: GB2262
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-337 <HEI>
 A;Cross-references: UNIPROT: Q9KTG5; GB:AB004176; GB:AB003852; NID:99655385; PIDN:AAF9409
 C;Genetics:
 A;Gene: VC0937
 A;Map position: 1

Query Match 34.2%; Score 52; DB 2; Length 737;
 Best Local Similarity 39.4%; Pred. No. 18;
 Matches 13; Conservative 4; Mismatches 12; Indels 4; Gaps 1;

QY 3 PTSSSTKTKTQLE---HLLDLQMLNGINN 31
 Db 330 PKHPKPKASAQLEAVRNLRAELQMLNGINN 362

RESULT 19
 P95285 probable LysR-type regulator [imported] - Sinorhizobium meliloti (strain 1021) magaplasm C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C;accession: P95285 A;Authors: M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9885, 2001 A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95285 MUID:21396509; PMID:11481432 A;Accession: P95285 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-304 <COL> A;Cross-references: UNIPROT:Q930K5; GB:AB006469; PID:AAK64848.1; PID:914523262; SPDB:GR galibert, P.; Flanigan, T.M.; Long, S.R.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Belpela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelauré, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A95039; MUID:21368234; PMID:11474104 A;Contents: annotation C;Genetics: A;Gene: SMA0353 A;Genome: Plasmid

Query Match Score 51; DB 2; Length 304;
 Best Local Similarity 48.1%; Pred. No. 9.5%;
 Matches 13; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

Qy 7 STRKTKTQLE---HLLDLQMLNGINN 31
 Db 58 STRKPKTLEGRTVLAERSVNSGIDN 84

RESULT 20
 E70122 flagellar hook-associated protein (FlgK) homolog - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004 C;Accession: E70122 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, ; Bowman, C.; Garland, C.; Fujii, C.; Cotton, M.D.; Horst, K.; Hatch, B. Nature 390, 580-586, 1997 A;Authors: Smith, H.O.; Venter, J.C. A;Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*. A;Reference number: A70100; MUID:98065943; PMID:9403685 A;Accession: E70122 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-627 <COL> A;Cross-references: UNIPROT:P70595; GB:AB001129; PID:92688071; PMID:AAC6657 A;Experimental source: strain B31

Query Match Score 51; DB 2; Length 627;
 Best Local Similarity 42.3%; Pred. No. 21%;
 Matches 11; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 5 SSSSTKTKTQLEHLLDLQMLNGINN 30
 Db 564 SBITKESSOSQILKXDLTDRMSISGVN 589

RESULT 21
 C70701 hypothetical protein Rv0029 - *Mycobacterium tuberculosis* (strain H37RV)
 C;Species: *Mycobacterium tuberculosis*
 C;Accession: C70701 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feitwell, T.; Gentle, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Shelton, S.; Squires, S. Nature 393, 537-544, 1998 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome A;Reference number: A70500; MUID:98295987; PMID:96244230 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-365 <COL> A;Cross-references: UNIPROT:P71599; GB:280233; PID:93261645; PMID:CA02414 A;Experimental source: strain H37RV C;Genetics: A;Gene: Rv0029

Query Match Score 50; DB 2; Length 365;
 Best Local Similarity 40.0%; Pred. No. 16%;
 Matches 12; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 2 APTSSSSPKKTKTQLEHLLDLQMLNGINN 31
 Db 43 AELNSNTAETATIAEHLKADLHRIVSGSAND 72

RESULT 22
 HB2447 DNA-binding response regulator VCA0532 [imported] - *Vibrio cholerae* (strain N16961 sero_ C;Species: *Vibrio cholerae* C;Accession: HB2447 R;Heidelberg, J.F.; Eisen, J.A.; Clayton, R.A.; Dodson, R.J.; chardson, D.; Brmoleieva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000 A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*. A;Reference number: A82035; MUID:2046833; PMID:10952301 A;Accession: HB2447 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-230 <HEI> A;Cross-references: UNIPROT:Q9RM56; GB:AB004184; GB:AB003853; NID:99657936; PIDN:AAF9643 A;Experimental source: serogroup O1; strain N16961; biotype El Tor C;Genetics: A;Gene: VCA0532 A;Map Position: 2 C;Superfamily: ompr protein; response regulator homology

Query Match Score 49; DB 2; Length 230;
 Best Local Similarity 40.3%; Pred. No. 14%;
 Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MAPTSSSSPKKTKTQLEHLLDLQMLNGIN 22
 Db 121 LAPSTESVEQTRFELDVLVDL 142

RESULT 23
 F82217 methyl-accepting chemotaxis protein VC1298 [imported] - *Vibrio cholerae* (strain N16961 s C;Species: *Vibrio cholerae* C;Accession: F82217 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Brmoleieva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000

A;Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Reference number: A32035; MUTD:20406833; PMID:1092301

A;Accession: F82217

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-543 <HEL>

A;Cross-references: UNIPROT:Q9KSF8; GB:AE004209; GB:AE003852; NID:99655779; PIDN:AAF9445

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC198

A;Map position: 1

Query Match 32.2%; Score 49; DB 2; Length 543;

Best Local Similarity 37.5%; Pred. No. 36;

Matches 9; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 4 TSSSTKKTQLOQEHLLIDLOMLIN 27

Db 506 SASETREISIDLEHLSQLESILN 529

RESULT 24

protein F52E1.4 [imported] - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001

C;Accession: A89130

A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biological processes

A;Reference number: A57000; MUTD:99069612; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans and www.Sanger.ac.uk/Projects/C_elegans

A;Accession: A89130

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1130 <SQL>

A;Cross-references: GB:chr_V; PIDN:AA837038.1; PID:91086805; GSPDB:GN00023; CESP:F52E1.4

C;Genetics:

A;Gene: F52E1.4

A;Map position: 5

C;Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain homolog

Query Match 32.2%; Score 49; DB 2; Length 1130;

Best Local Similarity 46.2%; Pred. No. 81;

Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 4 TSSSTKKTQLOQEHLLIDLOMLNGI 29

Db 906 TTASKCTPQVNLLNPLYTFDGI 931

RESULT 25

hypothetical protein F44G4.7 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T22210

A;Submitted to the EMBL Data Library, June 1995

A;Reference number: Z19530

A;Accession: T22210

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-240 <WIL>

A;Cross-references: UNIPROT:Q20417; EMBL:Z49910; PIDN:CRA90123.1; GSPDB:GN00020; CESP:F44G4.7

C;Genetics:

A;Gene: CESP:F44G4.7

A;Map position: 2

A;Introns: 123/2; 159/3

C;Superfamily: *Caenorhabditis elegans* hypothetical protein F44G4.7

Query Match 31.9%; Score 48.5; DB 2; Length 240;

Best Local Similarity 44.0%; Pred. No. 17;

Matches 11; Conservative 9; Mismatches 4;

Indels 1; Gaps 1;

Qy 3 PTSSSTKKTQLOQEHLLIDLOMLIN 27

Db 146 PTSSQEOREKWRVK-LIIDLEMILS 169

RESULT 26

H64307

hypothetical protein MJ0064 - *Methanococcus jannaschii*

C;Species: *Methanococcus jannaschii*

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C;Accession: H64307

R;Built: C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.;

i; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Marrick, J.M.; Giodek, A.;

rsen, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurbst, M.A.

Science 273, 1058-1073, 1996

A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.

A;Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*

A;Reference number: A64300; MUID:96337999; PMID:8688087

A;Accession: H64307

A;Cross-references: UNIPROT:Q60376; GB:U67464; GB:L77117; NID:G1590852; PIDN:AB98051.1;

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

C;Genetics:

A;Map position: FOR61888-62457

A;Start codon: GTG

Query Match 31.6%; Score 48; DB 2; Length 189;

Best Local Similarity 32.1%; Pred. No. 15;

Matches 9; Conservative 10; Mismatches 9;

Indels 0; Gaps 0;

Qy 4 TSSSTKKTQLOQEHLLIDLOMLINGIN 31

Db 22 SSSSVTEIVLDEELTKMLNLSEINN 49

RESULT 27

AB1367

aminopeptidase C [imported] - *Listeria monocytogenes* (strain EGD-e)

C;Species: *Listeria monocytogenes*

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C;Accession: AB1367

R;Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, R.; Dominguez-Bernal, G.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.H.; Jones, L.M.; Karst, U.; Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueño, E.; Maitouram, A.; Ma

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland,

A;Title: Comparative genomics of *Listeria* species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AB1367

A;Molecule type: DNA

A;Residues: 1-41 <GLA>

A;Cross-references: UNIPROT:069192; GB:NC_003210; PIDN:CADD00416.1; PMID:91611826; GSPDB:

C;Genetics:

A;Gene: pepC

C;Superfamily: aminopeptidase C (bleomycin hydrolase)

Query Match 31.5%; Score 48; DB 2; Length 441;

Best Local Similarity 34.6%; Pred. No. 40;

Matches 9; Conservative 7; Mismatches 10;

Indels 0; Gaps 0;

Qy 5 SSSTKKTQLOQEHLLIDLOMLNGIN 30

Db 344 TAMTKAERLDYKHSMLTHAMVLTGVN 369

RESULT 28
 AC1736 aminopeptidase C (imported) - Listeria innocua (strain CipI1262)
 C:Species: Listeria innocua
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AC1736
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez, Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, C.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karsch, U.;
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, B.; Maitouram, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A; Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AC1736
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-441 <GLA>
 A:Cross-references: UNIPROT:Q928V0; GB:AL592022; PIDN: CAC97659.1; PID: 916414954; GSPDB:G
 A:Experimental source: strain CipI1262
 C:Genetics:
 A:Gene: pepC
 C:Superfamily: aminopeptidase C (bleomycin hydrolase)

Query Match 31.6%; Score 48; DB 2; Length 441;
 Best Local Similarity 34.6%; Pred. No. 40;
 Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
 Qy 5 SSSTKKTQLQLEHLLDDQMLANGIN 30
 Db 344 TAVTKAERDLYDKHSMLTAVMLVGVN 369

RESULT 29
 JC8012 G protein-coupled neuropeptide pyrokinin-2 receptor (CG8795) - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004
 C:Accession: JC8012
 R:Rosenkilde, C.; Cazzamali, G.; Williamson, M.; Hauser, F.; Sondergaard, L.; Delotto, R.; Biochem. Biophys. Res. Commun. 309, 485-494, 2003
 A:Title: Molecular cloning, functional expression, and gene silencing of two Drosophila A:Reference number: JCS8011; PMID: 12951076
 A:Accession: JC8012
 A:Molecule type: mRNA
 A:Residues: 1-595 <ROS>
 A:Cross-references: GB:AY277899
 C:Comment: This receptor is a G protein-coupled receptor and a transmembrane protein as e. feeding, and behavior.
 C:Genetics:
 A:Gene: cg8795
 A:Introns: 115/1; 170/2; 214/3; 281/1; 357/3; 390/3
 C:Keywords: G protein-coupled receptor; neuropeptide pyrokinin; transmembrane protein

Query Match 31.6%; Score 48; DB 2; Length 595;
 Best Local Similarity 48.4%; Pred. No. 56;
 Matches 15; Conservative 3; Mismatches 9; Indels 4; Gaps 2;
 Qy 1 MAPTSSS-TKTKTQLQLEH--LLLDQMLIN 27
 Db 1 MLPNNSSGVLATDQLQFFNEKFLLNLTCVLN 31

RESULT 30
 GNLJG4 HIV-1 retropepsin (EC 3.4.23.16) - simian immunodeficiency virus (African green monkey) N Contains: endonuclease (EC 3.1...); retropepsin (EC 3.4.23.16); RNA-directed DNA poly C:Species: simian immunodeficiency virus, SIV
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 03-Jun-2002
 C:Accession: B30045
 R:Fuksawa, M.; Miura, T.; Hasegawa, A.; Morikawa, S.; Tsujimoto, H.; Miki, K.; Kitamura, Nature 333, 457-461, 1988
 A:Title: Sequence of simian immunodeficiency virus from African green monkey, a new memb

A:Reference number: A30045; MUID:88232906; PMID:3374586
 A:Accession: B30045
 A:Molecule type: DNA
 A:Residues: 1-1061 <PUK>
 A:Cross-references: EMBL:X07805; NID:961748; PID:gi1335593
 C:Comment: Specific enzymatic cleavages may yield mature proteins including protease, reverse transcriptase, and nucleotidyltransferase; polyprotein; reverse transcriptase; retropepsin
 C:Genetics:
 C:Superfamily: pol polyprotein
 C:Keywords: aspartic proteinase; hydrolase; nucleotidyltransferase; polyprotein; reverse transcriptase; retropepsin
 F:112/10/Product: retropepsin #status predicted <RTP>
 F:113/4/Active Site: Asp (shared with dimeric partner) #status predicted
 Query Match 31.6%; Score 48; DB 1; Length 1061;
 Best Local Similarity 52.9%; Pred. No. 1.1e+02;
 Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 Qy 11 TQLQLBHLDDQMLIN 27
 Db 976 TQLBQLQTKIQKILN 992

RESULT 31
 T11685 hypothetical protein SPBC21D10 13 SPBC1921.07C - fission yeast (Schizosaccharomyces pombe)
 A:Accession: T11685; T39791
 C:Date: 16-Jul-1999 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C:Accession: T11685; T39791
 R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 A:Submitted to the EMBL Data Library, September 1998
 A:Reference number: Z17313
 A:Accession: T11685
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-155 <SPB>
 A:Cross-references: UNIPROT:Q9USW9; EMBL:AL031536; NID:e1319499
 A:Experimental source: strain 972h(-)
 R:Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
 A:Submitted to the EMBL Data Library, October 1999
 A:Accession: T11685
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 129-244 <SE2>
 A:Cross-references: EMBL:AL1122033; PIDN: CAB58973.1; GSPDB:GN000067; SPDB:SPBC1921.07C
 A:Map Position: IIR
 A:Genetics:
 A:Note: intron positions not resolved (incomplete sequence)

Query Match 31.2%; Score 47.5; DB 2; Length 244;
 Best Local Similarity 45.8%; Pred. No. 24;
 Matches 11; Conservative 4; Mismatches 6; Indels 3; Gaps 1;
 Qy 4 TSSSTKTKTQLQLEHLLDDQMLIN 27
 Db 59 TSEBQK--ELEHTQSLMEN 79

RESULT 32
 P86548 polymorphic outer membrane protein B family (imported) - Chlamydophila pneumoniae (strain C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: P86548
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of chlamydial pneumoniae J138.
 A:Reference number: A86491; PMID:20330349; PMID:10871362
 A:Accession: P86548
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-938 <STO>

A; Cross-references: UNIPROT:Q9Z883; GB:BA000008; NID:98978835; PIDN:BA98772.1; GSPDB:GN
 A; Experimental source: strain J138
 C; Generics:
 A; Gene: pmp_15

Query Match 31.2%; Score 47.5; DB 2; Length 938;
 Best Local Similarity 42.9%; Pred. No. 1.1e+02;
 Matches 12; Conservative 4; Mismatches 9; Indels 3; Gaps 1;

Qy 3 PTSSSTKTT---QLQLEHLLDQMLIN 27
 Db 473 PTSSSTPTVGSTITLNHAIDLPSILS 500

RESULT 33

H72074 polymorphic membrane protein B/F family CP0286 [Imported] - Chlamydophila pneumoniae (strain N315) #sequence_change 09-Jul-2004
 C; Species: Chlamydophila pneumoniae; Chlamydia pneumoniae
 C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C; Accession: H72074; E81593
 R; Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
 A; Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
 A; Reference number: A720000; MUID:99206606; PMID:10192388
 A; Accession: H72074
 A; Molecule type: DNA
 A; Residues: 1-938 <KUR>
 A; Cross-references: UNIPROT:Q9Z883; GB:AE001631; GB:AE001363; PIDN:94376750; PIDN:AD1860
 A; Experimental source: strain CML029
 R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1405, 2000
 A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A; Reference number: A81500; MUID:20150255; PMID:10684935
 A; Accession: E81593
 A; Molecule type: DNA
 A; Residues: 1-938 <REF>
 A; Cross-references: GB:AE002190; GB:AE002161; NID:97189209; PIDN:AAF38143.1; PIDN:9718921
 A; Experimental source: strain AR39, HL cell18
 C; Generics:
 A; Gene: pmp_15; CP0286

Query Match 31.2%; Score 47.5; DB 2; Length 938;
 Best Local Similarity 42.9%; Pred. No. 1.1e+02;
 Matches 12; Conservative 4; Mismatches 9; Indels 3; Gaps 1;

Qy 3 PTSSSTKTT---QLQLEHLLDQMLIN 27
 Db 473 PTSSSTPTVGSTITLNHAIDLPSILS 500

RESULT 34

B70209 conserved hypothetical protein BBA18 - Lyme disease spirochete plasmid A/lp54
 C; Species: Borrelia burgdorferi (Lyme disease spirochete)
 C; Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
 C; Accession: B70209
 R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Hanlon, M.; Vugt, J.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Hatch, B.; Nature 390, 580-586, 1997
 A; Authors: Smith, H.O.; Venter, J.C.
 A; Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.
 A; Reference number: A70100; MUID:9806594; PMID:9403685
 A; Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-398 <KLE>
 A; Cross-references: UNIPROT:O5011; GB:AE000790; NID:92690224; PIDN:9269
 A; Accession: B70209
 A; Molecule type: DNA
 A; Residues: 1-398 <KLE>
 A; Experimental source: strain B31
 C; Generics:
 A; Gene: Plasmid
 C; Superfamily: Lyme disease spirochete plasmid

RESULT 35

P89839 hypothetical protein SA0640 [Imported] - *Staphylococcus aureus* (strain N315)
 C; Species: *Staphylococcus aureus*
 C; Accession: P89839
 C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001
 A; Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A; Reference number: A89758; MUID:21311952; PMID:11418146
 A; Accession: P89839
 A; Status: Preliminary
 A; Molecule type: DNA
 A; Residues: 1-557 <KUR>
 A; Cross-references: UNIPROT:Q99V76; GB:BA000018; PIDN:BA000018; PIDN:BA041873.1; GSPDB:G
 A; Experimental source: strain N315
 C; Generics:
 A; Gene: SA0640

Query Match 30.9%; Score 47; DB 2; Length 557;
 Best Local Similarity 58.8%; Pred. No. 72;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 12 QLQLEHLLDQMLIN 28
 Db 440 QLQLEHLLALERQIDDG 456

RESULT 36

T41244 SEC14 protein homolog SPCC23B6.04c - fission yeast (Schizosaccharomyces pombe)
 C; Species: Schizosaccharomyces pombe
 C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C; Accession: T41244
 R; Lyne, M.; Brown, S.; Quail, M.; Harris, D.; Rajandream, M.A.; Barrell, B.G.
 A; Reference number: Z21980
 A; Accession: T41244
 A; Status: Preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 1-1008 <LYN>
 A; Cross-references: UNIPROT:Q99U99; EMBL:AJ109608; PIDN:CAE51563.1; GSPDB:GN00068; SPDB:
 A; Experimental source: strain 972h-; cosmid c23B6
 C; Generics:
 A; Gene: SPDB:SPCC23B6.04C
 A; Map position: 3
 F; 639-822:Domain: cellular retinaldehyde-binding protein homology <CRB>
 A; Map position: 3
 Query Match 30.9%; Score 47; DB 2; Length 1008;
 Best Local Similarity 32.0%; Pred. No. 1.4e+02;
 Matches 8; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 3 PTSSSTKTTQLQLEHLLDQMLIN 27
 Db 702 PARQNTKTSPLQIRHLVPSLCAID 726

RESULT 37

A59282 nonmuscle myosin II heavy chain A - African clawed frog
 C; Species: Xenopus laevis (African clawed frog)

C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
 C;Accession: A59222
 R;Bhati,Dey, N.; Taira, M.; Conti, M.A.; Nooruddin, H.; Adelstein, R.S.
 Mech. Dev. 78, 33-36, 1998
 A;Title: Differential expression of non-muscle myosin heavy chain genes during Xenopus ϵ
 A;Reference number: A59282; MUID:90077683; PMID:985676
 A;Accession: A59282
 A;Superfamily: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-1964 <BRA>
 A;Cross-references: UNIPROT:093522; GB:AF055895; NIDN:93660671; PIDN: AAC83556.1; PID:9366
 A;Experimental source: cell line XTC
 C;Superfamily: myosin heavy chain; myosin motor domain homology <MMO>
 P;84-764/Domain: myosin motor domain homology <MMO>
 Query Match 30.9%: Score 47; DB 2; Length 1964;
 Best Local Similarity 42.9%; Pred. No. 3e+02;
 Matches 12; Conservative 2; Mismatches 14; Indels 0; Gaps 0;
 Qy 4 TSSSSTKTKQLQLEHLLIDQMLNGINN 31
 Db 196 TSHKSKKKGQGELRQLQIQNAPILEAFGN 223

RESULT 38
 T05656 Hypothetical Protein F22I13.50 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T05656
 R;Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.R
 Submitted to the Protein Sequence Database, February 1999
 A;Reference number: Z5420
 A;Accession: T05656
 A;Molecule type: DNA
 A;Residues: 1-159 <BEV>
 A;Cross-references: UNIPROT:Q9SYF7; EMBL:AL035539
 A;Experimental source: cultivar Columbia; BAC clone F22I13
 C;Genetics:
 A;Map position: 4
 A;Introns: 117/1
 A;Note: F22I13.50
 C;Superfamily: Arabidopsis thaliana hypothetical protein F22I13.50

Query Match 30.6%: Score 46.5; DB 2; Length 159;
 Best Local Similarity 46.4%; Pred. No. 21;
 Matches 13; Conservative 3; Mismatches 9; Indels 3; Gaps 1;
 Qy 3 PRSSSTKTKTQLEHLLIDQMLNGIN 30
 Db 83 PTPRSK--LDWBERYLHQMLN 107

RESULT 39
 C84888 Hypothetical protein At2g45250 [Imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Accession: C84888
 R;Lin, X.; Kaul, S.; Rounsbly, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umavam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:1061797
 A;Accession:C84888
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-211 <STO>
 A;Cross-references: UNIPROT:O22147; GB:AB002093; NID:92583136; PIDN: AAB82645.1; GSPDB:GN
 C;Generics:
 A;Gene: Atg45250
 A;Map position: 2

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